

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2005, 10:05:32 ; Search time 86 Seconds
(without alignments)
1244.472 Million cell updates/sec

Title: US-09-980-758A-8
Perfect score: 1045
Sequence: 1 PRDLPNPREKXMSERREL.....NFDIVNDEPLEGRYKWDRLX 209

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_prot:*
2: uniprot_tmbl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	969	92.7	196	2 Q9LJL5	Q9LJL5 arabidopsis
2	347.5	33.3	195	2 Q94CL9	Q94CL9 arabidopsis
3	346.5	33.2	195	2 Q9FX90	Q9FX90 arabidopsis
4	285	27.3	60	2 Q8W2K3	Q8W2K3 arabidopsis
5	187	17.9	192	2 Q9RS28	Q9RS28 pieum sativ
6	179	17.1	166	2 Q6T2Z0	Q6T2Z0 glycine max
7	179	17.1	207	2 Q8GUA2	Q8GUA2 nicotiana t
8	177	16.9	209	2 Q9SCR2	Q9SCR2 arabidopsis
9	176.5	16.9	191	2 O04154	O04154 arabidopsis
10	175.5	16.8	191	2 O82809	O82809 arabidopsis
11	175.5	16.8	191	2 O8LDX1	O8LDX1 arabidopsis
12	172	16.5	286	2 Q94CM0	Q94CM0 arabidopsis
13	169	16.2	205	2 Q6T2Z3	Q6T2Z3 glycine max
14	168.5	16.1	196	2 O48597	O48597 chenopodium
15	167	16.0	286	2 Q8GTJ3	Q8GTJ3 arabidopsis
16	164.5	15.7	185	2 Q8GT28	Q8GT28 lycopersico
17	162.5	15.6	289	2 Q48846	Q48846 arabidopsis
18	161	15.4	198	2 Q6T2Z2	Q6T2Z2 glycine max
19	156.5	15.0	500	1 GAR2_SCHPO	P41891 schizosacch
20	153.5	14.7	180	2 Q6T2Z1	Q6T2Z1 glycine max
21	153	14.6	262	2 Q6Z6G5	Q6Z6G5 oryza sativ
22	152	14.5	222	2 Q9PKB5	Q9PKB5 arabidopsis
23	145.5	13.9	210	2 Q8GT29	Q8GT29 lycopersico
24	144	13.8	242	2 Q7XDH8	Q7XDH8 oryza sativ
25	144	13.8	242	2 Q9FW65	Q9FW65 oryza sativ
26	143.5	13.7	396	2 Q754G3	Q754G3 ashbya goes
27	138.5	13.3	406	1 SR40_YEAST	P32583 saccharomyc
28	132.5	12.7	414	1 NSR1_YEAST	P27476 saccharomyc
29	132.5	12.7	451	2 Q9P785	Q9P785 schizosacch
30	132.5	12.7	2271	2 Q99QY4	Q99QY4 staphylococ
31	132.5	12.7	2271	2 Q7A362	Q7A362 staphylococ

Query Match 92.7%; Score 969; DB 2; Length 196;

Best Local Similarity 99.5%; Pred. No. 1.4e-54;

Matches 195; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

32 131.5 12.6 1241 2 Q75JC0
33 131 12.5 412 2 Q6MFI1
34 131 12.5 471 2 Q7RZG9
35 130.5 12.5 371 2 Q6FTH7
36 129.5 12.4 163 2 Q93V92
37 128 12.2 156 2 Q93VF6
38 128 12.2 189 2 Q9LRY0
39 128 12.2 600 2 Q90237
40 128 12.2 680 2 Q92033
41 127.5 12.2 455 2 Q86A18
42 127 12.2 1444 2 Q9VTN2
43 127 12.2 1514 2 Q8SY55
44 126.5 12.1 2275 2 Q8NUJ3
45 126.5 12.1 2275 2 Q6G620

ALIGNMENTS

RESULT 1

Q9LJL5 PRELIMINARY; PRT; 196 AA.
AC Q9LJL5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Gb|AAC23758.1 (Cyclin-dependent kinase inhibitor 6).
GN Name=ACK1; Synonyms=krp6;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20363099; PubMed=10907853;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety Pl,
RT TAC and BAC clones."
RL DNA Res. 7:217-221(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RN [3]
RP Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Park S.C., Cho J.W.;
RN [5]
RP Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA MEDLINE=21342510; PubMed=11449057;
RN [7]
RP de Veylder L., Beeckman T., Beeckman G.T.S., Krols L., Terras F.,
RN [8]
RA Landrieu I., Van Der Schueren E., Maes S., Nautes M., Inze D.;
RN [9]
RT "Functional analysis of Cyclin-dependent kinase inhibitors of
RT Arabidopsis."
RL Plant Cell 13:1653-1668(2001).
RN [10]
RP EMBL; AF000419; BAB02955.1; -
RN [11]
RP EMBL; AF106705; AAF77612.2; -
RN [12]
RP EMBL; AJ301557; CAC41620.1; -
RN [13]
RP GO; GO:0003634; Cinnuleus; IEA.
RN [14]
RP GO; GO:0004861; F.cyclin-dependent protein kinase inhibitor a...; IEA.
RN [15]
RP GO; GO:0016301; F.kinase activity; IEA.
RN [16]
RP GO; GO:0007050; P:cell cycle arrest; IEA.
RN [17]
RP InterPro; IPR003175; CDI.
RN [18]
RP Pfam; PF02334; CDI; 1.
RN [19]
RP Cyclin; Kinase.
RN [20]
RP SEQUENCE 196 AA; 21454 MW; ACS43304CE5B92C4 CRC64;

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QY 13 MSERKRELAEEASSTSFSPKTKTKLNDSSDPDSDHVDVIVFAVSSSSVASSAALASDCS 72
Db 1 MSERKRELAEEASSTSFSPKTKTKLNDSSDPDSDHVDVIVFAVSSSSVASSAALASDCS 60
QY 73 VTIGGEESDQSSISSGGCTSSKEIAKNSSFGVDLEDHQIETETETSTFTTSNFRKET 132
Db 61 VTIGGEESDQSSISSGGCTSSKEIAKNSSFGVDLEDHQIETETETSTFTTSNFRKET 120
QY 133 SPVSEGLGTTTTEMESSATKRGKQGVKPTPTAAETDLFSELESPDDKKQFIEKYNFD 192
Db 121 SPVSEGLGTTTTEMESSATKRGKQGVKPTPTAAETDLFSELESPDDKKQFIEKYNFD 180
QY 193 IVNDEPLEGRYKWDRL 208
Db 181 IVNDEPLEGRYKWDRL 196
RESULT 2
Q94CL9 PRELIMINARY; PRT; 195 AA.
AC Q94CL9;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Cyclin-dependent kinase inhibitor 7.
GN Name=kfp7;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21342510; PubMed=11449057;
RA de Veylder L., Beeckman T., Bemster G.T.S., Krols L., Terras F.,
RA Landrieu I., Van der Schueren E., Maes S., Naudts M., Inze D.;
RT "Functional analysis of Cyclin-dependent kinase inhibitors of
RT Arabidopsis.";
RL Plant Cell 13:1653-1668(2001).
DR EMBL; AJ301558; CAC41621.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0007050; P:cell cycle arrest; IEA.
DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.
KW Cyclin; Kinase.
SQ SEQUENCE 195 AA; 2208 MW; 60B81B47B752F6DF CRC64;
Query Match 33.3%; Score 347.5; DB 2; Length 195;
Best Local Similarity 45.4%; Pred. No. 8e-15;
Matches 93; Conservative 28; Mismatches 57; Indels 27; Gaps 10;
QY 13 MSERKRELAEEASSTSFSPKTKTKLNDSSD--SSPDSDHVDVIVFAVSSSSVASSAALASDE 70
Db 1 MSETKPKRDSVEG--SNIKMRLLDDDDVLRSPTR-----TLSSSSSSSLAYSVD 51
QY 71 ---CSVTIGGEESD-QSSISSGGCTSSKEIAKNSSFGVDLEDHQIETETETSTFTTS 126
Db 52 GGFCVALSEEDDHLSSISGGCSSSETNEIATLPF--SDLEAHEI-SETEISTLLTN 108
QY 127 NFRKETSVPVSEGLGET-----TTMESSATKRGKQGVKPTPTAAETDLFSELESDD 180
Db 109 NFRKQGISSENGLGTAEMDSATTEMRDQRKTEKKK-MEKSPTQAEILDFFSAAERYE- 166
QY 181 KKKQFIEKYNFIVNDEPLEGRYK 205
Db 167 -QKRFTKYNIVNDTPLEGRYQW 190
RESULT 3
Q9FX90 PRELIMINARY; PRT; 195 AA.
ID Q9FX90
QY 13 MSERKRELAEEASSTSFSPKTKTKLNDSSD--SSPDSDHVDVIVFAVSSSSVASSAALASDE 70
Db 1 MSETKPKRDSVEG--SNIKMRLLDDDDVLRSPTR-----TLSSSSSSSLAYSVD 51
QY 71 ---CSVTIGGEESD-QSSISSGGCTSSKEIAKNSSFGVDLEDHQIETETETSTFTTS 126
Db 52 GGFCVALSEEDDHLSSISGGCSSSETNEIATLPF--SDLEAHEI-SETEISTLLTN 108
QY 127 NFRKETSVPVSEGLGET-----TTMESSATKRGKQGVKPTPTAAETDLFSELESDD 180
Db 109 NFRKQGISSENGLGTAEMDSATTEMRDQRKTEKKK-MEKSPTQAEILDFFSAAERYE- 166
QY 181 KKKQFIEKYNFIVNDEPLEGRYK 205
Db 167 -QKRFTKYNIVNDTPLEGRYQW 190
RESULT 4
Q8W2K3 PRELIMINARY; PRT; 60 AA.
ID Q8W2K3
AC Q8W2K3;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Cyclin-dependent kinase inhibitor p22ack1 (Fragment).
GN Name=ACK1;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX Cho J.W., Park S.C.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF208692; AAL35985.1; -.
DR GO; GO:0016301; F:kinase activity; IEA.
KW Cyclin; Kinase.
FT NON_TER 60
SQ SEQUENCE 60 AA; 6268 MW; D0DE7D7DBD0472A1 CRC64;
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AC Q9FX90;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE F14J22.14 protein.
GN Name=F14J22.14;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
RA Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,
RA Lueros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
RA Walker M., Yu G., Ecker J., Theologos A., Davis R.W.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC011807; AAG13048.1; -.
DR PIR; H96532; H96532.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.
DR GO; GO:0007050; P:cell cycle arrest; IEA.
DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.
SQ SEQUENCE 195 AA; 21965 MW; 6A7E0867B752E5FF CRC64;
Query Match 33.2%; Score 346.5; DB 2; Length 195;
Best Local Similarity 45.4%; Pred. No. 9.2e-15;
Matches 93; Conservative 27; Mismatches 58; Indels 27; Gaps 10;
QY 13 MSERKRELAEEASSTSFSPKTKTKLNDSSD--SSPDSDHVDVIVFAVSSSSVASSAALASDE 70
Db 1 MSETKPKRDSVEG--SNIKMRLLDDDDVLRSPTR-----TLSSSSSSSLAYSVD 51
QY 71 ---CSVTIGGEESD-QSSISSGGCTSSKEIAKNSSFGVDLEDHQIETETETSTFTTS 126
Db 52 GGFCVALSEEDDHLSSISGGCSSSETNEIATLPF--SDLEAHEI-SETEISTLLTN 108
QY 127 NFRKETSVPVSEGLGET-----TTMESSATKRGKQGVKPTPTAAETDLFSELESDD 180
Db 109 NFRKQGISSENGLGTAEMDSATTEMRDQRKTEKKK-MEKSPTQAEILDFFSAAERYE- 166
QY 181 KKKQFIEKYNFIVNDEPLEGRYK 205
Db 167 -QKRFTKYNIVNDTPLEGRYQW 190
RESULT 4
Q8W2K3 PRELIMINARY; PRT; 60 AA.
ID Q8W2K3
AC Q8W2K3;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Cyclin-dependent kinase inhibitor p22ack1 (Fragment).
GN Name=ACK1;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX Cho J.W., Park S.C.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF208692; AAL35985.1; -.
DR GO; GO:0016301; F:kinase activity; IEA.
KW Cyclin; Kinase.
FT NON_TER 60
SQ SEQUENCE 60 AA; 6268 MW; D0DE7D7DBD0472A1 CRC64;
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Query Match 27.3%; Score 285; DB 2; Length 60;
 Best Local Similarity 100.0%; Pred. No. 1.9e-11;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 MSERKRELAEEASTSFSPKTKTKLNDSSDSSPDSDHVDIVFAVSSSSVASSAALASDECS 72
 Db 1 MSERKRELAEEASTSFSPKTKTKLNDSSDSSPDSDHVDIVFAVSSSSVASSAALASDECS 60

RESULT 5
 Q9FS28 ID Q9FS28 PRELIMINARY; PRT; 192 AA.
 AC Q9FS28;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Cyclin dependent kinase inhibitor.
 GN Name=Cki;
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
 OX NCBI_TaxID=3888;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Axillary bud;
 RA Shimizu-Sato S., Mori H.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RE EMBL; AB029483; BAB20860.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.
 DR GO; GO:0016301; F:kinase activity; IEA.
 DR GO; GO:0007050; P:cell cycle arrest; IEA.
 DR InterPro; IPR003175; CDI.
 DR Pfam; PF02234; CDI; 1.
 DR Cyclin; Kinase.
 KW Cyclin; Kinase.
 SQ SEQUENCE 192 AA; 21921 MW; E76D734000885EB2 CRC64;

Query Match 17.9%; Score 187; DB 2; Length 192;
 Best Local Similarity 30.7%; Pred. No. 0.00014;
 Matches 59; Conservative 30; Mismatches 83; Indels 20; Gaps 6;

QY 20 LAAEASTSFSPKTKTKLNDSSDSSPDSDHVDIVFAVSSSSVAS--SAALASDCSVTIGG 77
 Db 16 LAAEASTSPRTTKRKINENRK-----FSTVKPIATVRPETVTEKHSSTSD 67

QY 78 EESDQSSISSGCTSESKEIAKNSSGFVDLEDHQIETETSTFTTSNFRKTSFVSE 137
 Db 68 EEPFASCCSNGSVDELDEERK-----SLDLEVESAGTSTCNCDDEEREMRSSE 121

QY 138 GLGETTEMESSEATRKQ-PGVRKTPATAAEIEDLFSELESPDDKKQKFIKYNFIDVND 196
 Db 122 FRG-NGSHELESMTNSRRPISPPKTPTEVELEFFAAAEK--DIQKKFQEKYNDILKD 178

QY 197 EPLEGKYKNDRL 208
 Db 179 VPLEGREYVQL 190

RESULT 6
 Q6T220 ID Q6T220 PRELIMINARY; PRT; 166 AA.
 AC Q6T220;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Cyclin-dependent kinase inhibitor 2;2 (Fragment).
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Li S., Reverdatto S., Nielsen N.C.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RE EMBL; AY439104; AAS13377.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.
 DR GO; GO:0016301; F:kinase activity; IEA.
 DR GO; GO:0007050; P:cell cycle arrest; IEA.
 DR InterPro; IPR003175; CDI.
 DR Pfam; PF02234; CDI; 1.
 DR Cyclin; Kinase.
 KW Cyclin; Kinase.
 SQ SEQUENCE 166 AA; 18850 MW; 40FB19CF72A8A640 CRC64;

Query Match 17.1%; Score 179; DB 2; Length 166;
 Best Local Similarity 34.9%; Pred. No. 0.00039;
 Matches 60; Conservative 28; Mismatches 58; Indels 26; Gaps 10;

QY 40 SPDSPSDHVDIVFAVSSSSVASSAALASDECSVTIGGESDSSISGCTFSESKEIA 99
 Db 18 ASASSPRRKISFVQKSLSNATSP--TTEE---RISG-ESPASCCSNGSFDENR-II 70

QY 100 KNSSSFGVDLEDHQIETET-ETSTFTTSNFRKTSFVSEGLGETTEMESSE--ATKRKQ 156
 Db 71 KSSD---LEVESAQVETWTCNCGEQQQKIRREMS-----LTREVDSTEEHITKTS 119

QY 157 PGVRKTPATAAEIEDLFSELESPDDKKQKFIKYNFIDVNDPLEGKYKNDRL 208
 Db 120 ---RCVPTSELEDDFFAAAEK--DIQKRTDKYNDYFVKDMPLEGREYVQL 166

RESULT 7
 Q8GUA2 ID Q8GUA2 PRELIMINARY; PRT; 207 AA.
 AC Q8GUA2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Cyclin-dependent kinase inhibitor.
 GN Name=kis2;
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Jasinski S., Saraiva Leite C., Domenichini S., Stevens R., Raynaud C.,
 RA Peremes C., Bergounioux C., Glab N.;
 RT "NtKIS2, a novel tobacco cyclin-dependent kinase inhibitor
 RT differentially expressed during the cell cycle and plant
 RT development.";
 RL Plant Physiol. Biochem. 41:667-676(2003).
 DR EMBL; AJ517189; CAD56868.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.
 DR GO; GO:0016301; F:kinase activity; IEA.
 DR GO; GO:0007050; P:cell cycle arrest; IEA.
 DR InterPro; IPR003175; CDI.
 DR Pfam; PF02234; CDI; 1.
 DR Cyclin; Kinase.
 KW Cyclin; Kinase.
 SQ SEQUENCE 207 AA; 23278 MW; F5AE70AD2261BC2D CRC64;

Query Match 17.1%; Score 179; DB 2; Length 207;
 Best Local Similarity 28.6%; Pred. No. 0.00051;
 Matches 58; Conservative 30; Mismatches 81; Indels 34; Gaps 8;

QY 11 KXMSERKRELAEEASTSFSPKTKTKLNDSS--DSSPD-----SHDVIVFAVSSSSVASSA 64
 Db 28 KMTASAEREVLVADHA-----KKRKWCDDLEMLPTVACVRSHSDILVAQESLVTPTS 82

QY 65 ALASDCSVTIGGESDQSSISGCTFSESKEIAKNSSGFVDLEDHQIETETSTFTFI 124

Db 83 ELSKPKENAAL---SSDFDALLASCC-----ASNGSSKSLDLLEETVEIATSKS--- 128
QY 125 TSNFRKETSVPSEGLGETTETEMESSATKRQKQGVKRTPTAAEIRDLPSLESPDDKKKQ 184
Db 129 -----KESIKAEIRQMEPTTRAHPKRRRLTE--EKMPSETDLEEFFAAAK--DILKR 179
QY 185 FIEKYNFDIVNDEPLEGRYKWR 207
Db 180 FTKYKYNFDFVKEEPLGHEWVR 202

RESULT 8
Q9SCR2 PRELIMINARY; PRT; 209 AA.

AC Q9SCR2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein T3A5.10 (Cdc2a-interacting protein) (Hypothetical protein At3g50630).
GN Name:T3A5.10; Synonyms=At3g50630, ICK2;
OS Arabidopsis thaliana (Mouse-ear cress);
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bloeker H., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22088475; PubMed=120933376;
RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome annotation."
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
RN [4]
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=20224033; PubMed=10758489;
RA Lui H., Wang H., DeLong C., Fowke L.C., Crosby W.L., Robert P.R.;
RT "The Arabidopsis Cdc2a-interacting protein ICK2 is structurally related to ICK1 and is a potent inhibitor of cyclin-dependent kinase activity in vitro."
RL Plant J. 21:379-385(2000).
RN [6]
RP SEQUENCE FROM N.A.
RA Totoki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A., Narusaka M., Shin-i T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y., Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K., Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J., Hayaishizaki Y., Shinozaki K.;
RT "Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs."
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
DR EMBL; ALI32979; CAB62432.1; -
DR EMBL; AY088290; AAM65829.1; -
DR EMBL; AJ251851; CAB76424.1; -
DR EMBL; AK176528; BAD44291.1; -
DR EMBL; AK176728; BAD44491.1; -
DR PIR; T46140; T46140.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.

DR GO; GO:0007050; P:cell cycle arrest; IEA.
DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.
KW Hypothetical protein.
SQ SEQUENCE 209 AA; 24036 MW; 0B5EEFE9ED256B53 CRC64;

Query Match 16.9%; Score 177; DB 2; Length 209;
Best Local Similarity 30.7%; Pred. No. 0.0007;
Matches 65; Conservative 44; Mismatches 73; Indels 30; Gaps 13;

QY 16 RKRELAEEASSTSPSPKTKLNDSSDSDSPSHDVIVFAVSSSS-----VASSAALASDEC 71
Db 7 RERDVVEENGVT-TTVKRRKVEVD-LVESRIILSPCVQATNRGGIVARNASAGSETS 64
QY 72 SVTIGGEES-----DOSSSISSGCFTSESKEIAKNSSSFGVDLEDHQ-IEETET 120
Db 65 VIVVRRRSPVPEQCQIEEDSSVSC--CTSEEK--SKRIEF-VDLNENGGDDRETET 120
QY 121 STFITSNFRKETSVPSEGLGETTETEMESSATKRQKQGVKRTPTAAEIEDLFSELESPPD 180
Db 121 S-WIYDDLK--SEESNMNDSSVAVEDVESRRRLRKLHETVKEAELEDFQVAEK--D 175
QY 181 KKKQFIE---KYNEDIVNDEPL-BGRYKWDRL 208
Db 176 LRNLKLECSMKYNFDFEKDEPLGGRYEWVKL 207

RESULT 9
Q04154 PRELIMINARY; PRT; 191 AA.

AC Q04154;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cyclin-dependent kinase inhibitor protein.
GN Name=ICK1;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Columbia;
RX MEDLINE=97242401; PubMed=9087400;
RA Wang H., Fowke L.C., Crosby W.L.;
RT "A plant cyclin-dependent kinase inhibitor gene."
RL Nature 386:451-452(1997).
DR EMBL; U94772; AAC49698.1; -
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0007050; P:cell cycle arrest; IEA.
DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.
KW Cyclin; Kinase.
SQ SEQUENCE 191 AA; 22239 MW; 0432BD4F626C07B5 CRC64;

Query Match 16.9%; Score 176.5; DB 2; Length 191;
Best Local Similarity 26.7%; Pred. No. 0.00067;
Matches 59; Conservative 34; Mismatches 63; Indels 65; Gaps 9;

QY 16 RKRELAEEASSTSPSPKTKLNDSSDSDSPSHDVIVFAVSSSSVASSAALASDECSTVI 75
Db 7 KAKGIVEAGVSTYMLRSR-----IVVRSKS-----SSVSV 41
QY 76 GGEESDQSSSISSGCFTSESKEIAKNSSSFGVDLEDHQIEETETSTF-----ITSNF 128
Db 42 VGD-----NGVSSSC--SGSNEYKKEL---IHLSEEDKDGDTETSTVRRGTRKRLCENL 91
QY 129 RKE-----TSPVSEGL-----GETTEMSSATKRQKQGVKRTPTAAE 167
Db 92 REEREKEIKSMENYSSSEFSAVKSLSLCCSCSGRKTMEETVTAEEEEKAKUMTEPTESE 151

QY 168 IEDLFSESPDDKKQFIEKYNFDIVNDEPLEGRYKWDRL 208
 Db 152 IEDFFVEAEK--QLKEKFKKYNFDFEKEKPLEGRYEWVKL 190

RESULT 10

O82809 ID O82809 PRELIMINARY; PRT; 191 AA.
 AC O82809
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Cyclin-dependent kinase inhibitor.
 GN Name=ICK1; Synonyms=A2923430;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RX MEDLINE=98426383; PubMed=9753775;
 RA Wang H., Qi Q., Schorr P., Cutler A.J., Crosby W.L., Fowke L.C.;
 RT "ICK1, a cyclin-dependent protein kinase inhibitor from Arabidopsis
 RT thaliana interacts with both Cdc2a and CycD3, and its expression is
 RT induced by abscisic acid";
 RL Plant J. 15:501-510(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Rounsley S.D., Kaul S., Lin X., Ketchum K.A., Crosby M.L.,
 RA Brandon R.C., Sykes S.M., Mason T.M., Kerlavage A.R., Adams M.D.,
 RA Somerville C.R., Venter J.C.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Town C.D., Kaul S.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC003040; AAC23758.1; -;
 DR EMBL; AF079587; AAC34660.1; -;
 DR PIR; T01132; T01132.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . . ; IEA.
 DR GO; GO:0016301; F:kinase activity; IEA.
 DR GO; GO:0007050; P:cell cycle arrest; IEA.
 DR InterPro; IPR003175; CDI.
 DR Pfam; PF02234; CDI; 1.
 KW Cyclin; Kinase.
 SQ SEQUENCE 191 AA; 22283 MW; 0477A91E277C46B2 CRC64;

Query Match 16.8%; Score 175.5; DB 2; Length 191;
 Best Local Similarity 26.7%; Pred. No. 0.00078;
 Matches 59; Conservative 34; Mismatches 63; Indels 65; Gaps 9;

QY 16 KRELAEASSTFSPLKTKLNDSSDPSHDVIVFAVSSSVASSAALASDECSTI 75
 Db 7 KARGIVEAGVSTYMLRSRR-----IVYRSEKS-----SSVSV 41
 QY 76 GGESDQSSISGCGTSSKEIAKNSSPGVLEHDHQTETSTF-----ITSNF 128
 Db 42 VGD-----NGVSSSC--SGSNEYKKEL-----IHLEEDKGDGTETSTYRGTGKRLFENL 91
 QY 129 RKE-----TSPVSEGL-----GETTMESSATKRKQPGVKPTAAE 167
 Db 92 REEKEELSKSMENYSSEFSAVKESLDCCSGRKTWEETVTAEEBKAKLMTMPTESE 151
 QY 168 IEDLFSESPDDKKQFIEKYNFDIVNDEPLEGRYKWDRL 208
 Db 152 IEDFFVEAEK--QLKEKFKKYNFDFEKEKPLEGRYEWVKL 190

RESULT 11

QY 168 IEDLFSESPDDKKQFIEKYNFDIVNDEPLEGRYKWDRL 208
 Db 152 IEDFFVEAEK--QLKEKFKKYNFDFEKEKPLEGRYEWVKL 190

RESULT 12

Q94CM0 ID Q94CM0 PRELIMINARY; PRT; 286 AA.
 AC Q94CM0
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Cyclin-dependent kinase inhibitor 4.
 GN Name=ktp4;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21342510; PubMed=11449057;

Q8LDX1

ID Q8LDX1 PRELIMINARY; PRT; 191 AA.
 AC Q8LDX1
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cyclin-dependent kinase inhibitor protein.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2208475; PubMed=12093376;
 RA Haas B.J., Volkovsky N., Town C.D., Troukhan M., Alexandrov N.,
 RA Feldmann K.A., White R.B., White O., Salzberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 RT annotation";
 RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY085749; AM62967.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . . ; IEA.
 DR GO; GO:0016301; F:kinase activity; IEA.
 DR GO; GO:0007050; P:cell cycle arrest; IEA.
 DR InterPro; IPR003175; CDI.
 DR Pfam; PF02234; CDI; 1.
 KW Cyclin; Kinase.
 SQ SEQUENCE 191 AA; 22282 MW; 19B7A91E277C46B2 CRC64;

Query Match 16.8%; Score 175.5; DB 2; Length 191;
 Best Local Similarity 26.7%; Pred. No. 0.00078;
 Matches 59; Conservative 34; Mismatches 63; Indels 65; Gaps 9;

QY 16 KRELAEASSTFSPLKTKLNDSSDPSHDVIVFAVSSSVASSAALASDECSTI 75
 Db 7 KARGIVEAGVSTYMLRSRR-----IVYRSEKS-----SSVSV 41
 QY 76 GGESDQSSISGCGTSSKEIAKNSSPGVLEHDHQTETSTF-----ITSNF 128
 Db 42 VGD-----NGVSSSC--SGSNEYKKEL-----IHLEEDKGDGTETSTYRGTGKRLFENL 91
 QY 129 RKE-----TSPVSEGL-----GETTMESSATKRKQPGVKPTAAE 167
 Db 92 REEKEELSKSMENYSSEFSAVKESLDCCSGRKTWEETVTAEEBKAKLMTMPTESE 151
 QY 168 IEDLFSESPDDKKQFIEKYNFDIVNDEPLEGRYKWDRL 208
 Db 152 IEDFFVEAEK--QLKEKFKKYNFDFEKEKPLEGRYEWVKL 190

de Veylder L., Beekman T., Beemster G.T.S., Krols L., Terras F., Landrieu I., Van Der Schueren E., Maes S., Naudts M., Inze D.; "Functional analysis of cyclin-dependent kinase inhibitors of Arabidopsis.", Plant Cell 13:1653-1668 (2001).

EMBL; AJ301555; CAC41618.1; -.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.

GO; GO:0016301; F:kinase activity; IEA.

GO; GO:0007050; P:cell cycle arrest; IEA.

InterPro; IPR003175; CDI.

Pfam; PF02234; CDI; 1.

Cyclin; Kinase.

SEQUENCE 286 AA; 31719 MW; 1CEBA472583302AAD CRC64;

Query Match	16.5%	Score 172;	DB 2;	Length 286;
Best Local Similarity	23.7%;	Pred. No. 0.0021;		
Matches	57;	Conservative 44;	Mismatches 80;	Indels 60; Gaps 9;
Qy	1 PRDLP-----KNPREKOWSERKEALAEASS-----TSFSPKKTKL 37			
Ddb	71 PSSLPPTSGNPPSKQMVKMKQQQNMDCGYQLRSRLQKKPPIVWIRSTKRKQRR 130			
Qy	38 NDSSDSGPDGHVIVFAVVSSSVASSAALASDECSTVIGEESSDOSSSISSCGFTSESKE 97			
Ddb	131 NETGRNPNRPS-----NDSTRGDGSRSDSVESVFGDKDLISEIN----- 174			
Qy	98 IAKNSSSFG---VDLEHQLIETETSTETITSFRKE--TSPVSEB----LGTTTTME 147			
Ddb	175 ---KDPTGGNFDFLEBEHTQRTTRSTPCSLRPRPEIMTTGCSSTKLNI CVESNQRED 231			
Qy	148 SSSATKRQPGVRTPTTAABIEDLFSELSPDDKKQFIETKNFYDVANDEPLEGRYKWDR 207			
Ddb	232 SLRSRHRR-----PTTPMEDFFSGAE--EEQQKFIEKNFYDPVNEQPLPCRFEWTK 283			
Qy	208 L 208			
Ddb	284 V 284			

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RESULT 13
Q6T223
Q6T223 PRELIMINARY; PRT; 205 AA.
Q6T223
Q6T223 AC
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cyclin-dependent kinase inhibitor 1;1.
OS Glycine max (soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurasids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
NCBI_TaxID=3847;
RN [1]
SEQUENCE FROM N.A.
Li S., Reverdatto S., Nielsen N.C.;
Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
EMBL; AY439101; AAS13374.1; -
GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0007050; P:cell cycle arrest; IEA.
DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.
DR Cyclin; Kinase.
SQ
SEQUENCE 205 AA; 22875 MW; 1B6F2D481710205E CRC64;

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Query Match 16.2%; Score 169; DB 2; Length 205;
Best Local Similarity 30.2%; Pred.No.0.0022;
Matches 61; Conservative 33; Mismatches 82; Indels 26; Gaps 9;

QY 20 LAEEASTSFSLKTKLNDSPDSDHDIIVFAVSSSVASSAALADECSVTIGGEE 79
|||||::: : ::::: |||||
|||::: : ::::: |||||

Db	15	LAMEAVSSAPSPSKRKKIINSTNQEPKSKTP--RTSSSSAVKPAITVEMRPVS-----	67
Qy	80	SDOSSISSCQFTSKEKEI-----AKNSSFGVD-----LEDHQIET-ETETSTFTITSN--	127
Db	68	---PEMWQRCLSPTSSEIPASCCSSNGSIGLDQDRIKLLDUEVESAQVETSTCNGGHEI	124
Qy	128	FRKETSPVSEGLGETTTEMESSATKRKQPGVRKT-PTAAEIBDLFSELESPDDKKKQFI	186
Db	125	ERREMKRSSE-LRENSQPEPEMEINSHRVLSKAKAMPTLELEEFPAASEK--DIQKRFO	181
Qy	187	EKYNFDIVNDEPLEGKYKWDRL	208
Db	182	DRYNDIVKDVPLEGRYEWVOL	203
RESULT	14		
O48597			
ID	O48597	PRELIMINARY;	PRT; 196 AA.

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RESULT 14
O48597 PRELIMINARY; PRT; 196 AA.
ID AC O48597;
DT DT 01-JUN-1998 (T-EMBLrel. 06, Created)
DT DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)
DT DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE DE Cyclin-dependent kinase inhibitor protein.
GN GN Name=CDK11;
OS OS Chenopodium rubrum (Red goosefoot) (Pigweed).
OC OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC OC Caryophyllales; Amaranthaceae; Chenopodium.
OX OX NCBI_TaxID=3560;
RN RN [1]
RP RP SEQUENCE FROM N.A.
RX RX MEDLINE=99329903; PubMed=10409053;
RA RA Fontain M.D., Renz A., Beck E.;
RT RT "Isolation of a cDNA encoding a G1-cyclin-dependent kinase inhibitor
RT RT from suspension-cultured photoautotrophic chenopodium rubrum cells.";
RL RL Plant Physiol. 120:339-339(1999).
DR DR EMBL; AJ002173; CAA05215.1; -.
DR DR PIR; T09968; T09968.
DR DR GO; GO:0005634; C:nucleus; IEA.
DR DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. .; IEA.
DR DR GO; GO:0016301; F:kinase activity; IEA.
DR DR GO; GO:0007050; P:cell cycle arrest; IEA.
DR DR InterPro; IPR003175; CDI.
DR DR Pfam; PF02234; CDI; 1.
DR DR Cytlin; Kinase.
SQ SQ SEQUENCE 196 AA; 21685 MW; 150349F7ED82A6B2 CRC64;

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Query Match	16.1%;	Score 168.5;	DB 2;	Length 196;
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Qy	20	LAEAGSTSPSPUKTKLNDSSD-----SSPDSHDVIVFAVSSSSSVASSAAL	66	
Db	1	MAAAAPTSS-SPAKKIKKYKSSYNIPQLSRKKLSAPEN-----FAELTTPLEVAAV	54	
Qy	67	ASDE-----CSVT--IGGESDQSSSSSGCF--TSEKIEIAKNSSSFGVDLEDHOIETE	117	
Db	55	VEEEVAVNCSSSEVITATRDPFPSCSNYDQLSSSEPEVVKDDDLGNRTADPESV--	113	
Qy	118	TETSTFTITSNFKRSTPVSGLGTTTTESSATKKQ-----PGVRKT-----P	163	
Db	114	-----GEASKQKESHRTEAREATKLDODYPATKSTVQIKMP	151	
Qy	164	TAAEIDLFSELSPDDKKQFIETKNFNDVNDPELEGYKW	205	
Db	152	SDSEIEEFFFAVASK--DLQRRFSEKFNFDIVKDVPLKGRYDW	191	

RESULT 15	
Q8GYJ3	
ID Q8GYJ3	PRELIMINARY;
AC Q8GYJ3;	PRT; 286 AA.
DT 01-MAR-2003	(TREMELrel. 23, Created)

Search completed: September 30, 2005, 11:35:34
Job time : 89 secs

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OM nucleic - nucleic search, using sw model

Run on: September 30, 2005, 09:05:51 ; Search time 3087 Seconds
(without alignments)
9826.033 Million cell updates/sec

Title: US-09-980-758A-7
Perfect score: 626
Sequence: 1 ctccgagattaccacaaat.....acaagtgggagtcgactttaa 626

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	626	100.0	626	6	BD267733
2	612.8	97.9	824	6	AX008797 Sequence
3	612.8	97.9	824	6	AX463066 Sequence
4	611.4	97.7	840	8	AF106705 Arabidops
5	589.4	94.2	591	8	AJ301557 Arabidops
6	335.8	53.6	81875	8	AF000419 Arabidops
7	204.4	32.7	4116	8	AF208692 Arabidops
8	122	19.5	588	8	AJ301558 Arabidops
9	122	19.5	642	6	AX008798 Sequence
10	122	19.5	642	6	AX463067 Sequence
11	58	9.3	7218	6	I66494 Sequence 14
12	53	8.5	927	8	AB029483 Pisum sat
13	49.6	7.9	597	8	AY439102 Glycine m
14	47.2	7.5	618	8	AY439101 Glycine m
15	46.6	7.4	104679	8	AC011807 Arabidops
16	46.4	7.4	499	8	AY439104 Glycine m
17	46.2	7.4	804	6	AX008805 Sequence
18	46.2	7.4	804	6	AX463073 Sequence
19	46.2	7.4	804	8	AJ002173 Chenopodi

20	45.8	7.3	377	6	AX008795	Sequence
21	45.8	7.3	377	6	AX463063	Sequence
22	45.8	7.3	443	6	AX008794	Sequence
23	45.8	7.3	443	6	AX463064	Sequence
24	45.8	7.3	660	6	AX008793	Sequence
25	45.8	7.3	660	6	AX463062	Sequence
26	45.8	7.3	780	8	AY085749	Arabidops
27	45.8	7.3	856	8	ATU94772	Arabidops
28	45.8	7.3	904	6	AX008791	Sequence
29	45.8	7.3	905	6	AX463060	Sequence
30	45.4	7.3	789	8	NT0297906	Sequence
31	45	7.2	225203	2	AC124569	Arabidops
32	44.6	7.1	861	8	ATH301555	Arabidops
33	44.6	7.1	870	6	CQ803830	Sequence
34	44.6	7.1	870	8	AF123315	Arabidops
35	44.6	7.1	1290	6	AX463075	Sequence
36	44.6	7.1	1341	8	AY087958	Arabidops
37	44.6	7.1	184458	2	AC141779	Apis mell
38	43.6	7.0	1312	8	AK117586	Arabidops
39	43.6	7.0	202882	10	AC139568	Mus muscu
40	43.4	6.9	1072	8	NTA517189	Nicotiana
41	43	6.9	533	6	AX008799	Sequence
42	43	6.9	533	6	AX463068	Sequence
43	43	6.9	669	6	CQ803834	Sequence
44	43	6.9	669	8	ATH301554	Arabidops
45	43	6.9	797	6	AX463079	Sequence

ALIGNMENTS

RESULT 1
BD267733

LOCUS

DEFINITION

BD267733 626 bp DNA linear PAR 17-JUL-2003
Method of promoting plant cell proliferation by functionally inhibiting plant cyclin inhibitor gene.

ACCESSION

BD267733.1 GI:33077501

VERSION

JP 2002543823-A/4.

KEYWORDS

Arabidopsis thaliana (thale cress)

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 626)

Roberts, J. and Kelly, B.

Method of promoting plant cell proliferation by functionally inhibiting plant cyclin inhibitor gene

Patent: JP 2002543823-A 4 24-DEC-2002;

PRED HUTCHINSON CANCER RESEARCH CENTER

OS Arabidopsis thaliana (thale cress)

PN JP 2002543823-A/4

PD 24-DEC-2002

PF 15-MAY-2000 JP 2000618299

PI 14-MAY-1999 US 60/134373

PC JAMES ROBERTS, BETH KELLY

promoting plant cell proliferation by functionally CC

inhibiting

CC plant cyclin inhibitor gene

PH Key Location/Qualifiers

FT source 1..626

FT /organism='Arabidopsis thaliana (thale cress)';

Location/Qualifiers

1..626

/organism='Arabidopsis thaliana'

/mol_type='genomic DNA'

/db_xref='taxon:3702'

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Query Match 100.0%; Score 626; DB 6; Length 626;

Best Local Similarity 100.0%; Pred. No. 5.8e-169;

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Db 1 CTCGAGATTACCCAAAAATCAAGAGAGAAAAAATGAGCGAGAGAAAGCGAGAGCTTG 60
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QY 181 CTTTCGTCGCGGCTTTAGCGTCTGATGAATGTTTCGTTACCATCGTGGAGAAAGATG 240
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QY 601 GTCGCTACAAAGTGGGATCGACTTTAA 626
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LOCUS AX008797 824 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 7 from Patent WO9964599.
ACCESSION AX008797
VERSION AX008797.1 GI:9996261
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Fowke, L.C., Wang, H. and Crosby, W.I.
Cyclin-dependent kinase inhibitors as plant growth regulators
Patent: WO 9964599-A 7 16-DEC-1999;
FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD
(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV
SASKATCHEWAN TECHNOLOGIES (CA)
Location/Qualifiers
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Best Local Similarity 99.7%; Pred. No. 3.7e-165;
Matches 614; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 11 ACCCAAAATCCAGAGAGAAAAAATGAGCGAGAGAAAGCGAGAGCTTGCAGAGAAGC 70
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QY 611 GTGGGATCGACTTTAA 626
Db 624 GTGGGATCGACTTTAA 639
RESULT 3
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LOCUS AX463066 824 bp DNA linear PAT 15-JUL-2002
DEFINITION Sequence 7 from Patent WO0250292.
ACCESSION AX463066
VERSION AX463066.1 GI:21886079
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Fowke, L.C., Wang, H. and Zhou, Y.
Modulation of plant cyclin-dependent kinase inhibitor activity
Patent: WO 0250292-A 7 27-JUN-2002;
Patent: WO 0250292-A 7 27-JUN-2002;
University of Saskatchewan Technologies (CA); Minister of
Agriculture and AgriFood Canada (CA)
Location/Qualifiers
1. .824
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"
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source
ORIGIN
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Query Match	97.9%;	Score 612.8;	DB 6;	Length 824;	
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DB	84	TTCAAGCACAAAGCTTCTCACCACTGAAGAAAACGAAGCTTAATGATTCTTCTGATTATC	143		
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QY	191	GGCTTTAGCGTCTGATGATGTTCCGTTACCACTGATCCATCGTGGAGAGAAAGTGCAGTCC	250		
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QY	251	GAGTATCAGCTCCGCTGTTTTCACCACTGATCCATCGTGGAGAGAAAGTGCAGTCC	310		
DB	264	GAGTATCAGCTCCGCTGTTTTCACCACTGATCCATCGTGGAGAGAAAGTGCAGTCC	323		
QY	311	GTGTTGTTAGTCTCGAGGATCATCAATCGAAACCGAAACCGAAACCTTCAACATTCAT	370		
DB	324	GTGTTGTTAGTCTCGAGGATCATCAATCGAAACCGAAACCGAAACCTTCAACATTCAT	383		
QY	371	CACCAGCAATTCAGAAAGAGAGCGAGTCCAGTGAAGAGGTTTCGGAGAAACGACAA	430		
DB	384	CACCAGCAATTCAGAAAGAGAGCGAGTCCAGTGAAGAGGTTTCGGAGAAACGACAA	443		
QY	431	AGAAATGGATCATCATCGGCAACGAGAGAAACCAACCGGGGTCGAGGAGTCCAA	490		
DB	444	AGAAATGGATCATCATCGGCAACGAGAGAAACCAACCGGGGTCGAGGAGTCCAA	503		
QY	491	GGCGGCGGAGATTGAGGATTTGTTCTCGGAGCTAGAGAGTCCAGACGATGAAGAGCA	550		
DB	504	GGCGGCGGAGATTGAGGATTTGTTCTCGGAGCTAGAGAGTCCAGACGATGAAGAGCA	563		
QY	551	ATTATAGAAAAGTACAACTTCGATATTGATGATGATGATGATGATGATGATGATGAT	610		
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DEFINITION	Arabidopsis thaliana cyclin dependent kinase inhibitor (ACK1) mRNA, complete cds.				
ACCESSION	AF106705				
VERSION	AF106705.2	GI:8789104			
KEYWORDS	Arabidopsis thaliana (thale cress)				
SOURCE	Arabidopsis thaliana				
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REFERENCE	1	(bases 1 to 840)			
AUTHORS	Park,S.C. and Cho,J.W.				
TITLE	A novel cyclin dependent kinase inhibitor (ack1)				
JOURNAL	Unpublished				
REFERENCE	2	(bases 379 to 789)			
AUTHORS	Park,S.C. and Cho,J.W.				
TITLE	Direct Submission				
JOURNAL	Submitted (14-NOV-1998) Kumho Life & Environmental Science				
REFERENCE	3	(bases 1 to 840)			

AUTHORS	Park,S.C. and Cho,J.W.				
TITLE	Direct Submission				
JOURNAL	Submitted (28-JUN-2000) Kumho Life & Environmental Science				
REMARK	Laboratory, 572 Sangamdong Kwangsanku, Kwangju 506-712, South Korea				
COMMENT	Sequence update by submitter				
FEATURES	On Jun 28, 2000 this sequence version replaced gi:8574522.				
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Query Match	97.7%;	Score 611.4;	DB 8;	Length 840;	
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DB	121	GGACTCTCATGAGCTCATGCTTTCGCGGTTTCATCTTCTTCGTTGCTTCGCGGCG	180		
QY	194	TTTAGGCTCTGATGATGTTTCGTTACCATCGTGGAGAGAAAGTGCAGTCCCTCGAG	253		
DB	181	TTTAGGCTCTGATGATGTTTCGTTACCATCGTGGAGAGAAAGTGCAGTCCCTCGAG	240		
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DB	361	GAGCAATTCAGAAAAGAGACGAGTCCAGTGAAGAGGTTTGGGAGAAACGACACAGA	420		
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RESULT 5
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LOCUS
DEFINITION
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  (krp6 gene).
ACCESSION
  AJ301557
VERSION
  AJ301557.1 GI:14422294
KEYWORDS
  cyclin-dependent kinase inhibitor; krp6 gene.
SOURCE
  Arabidopsis thaliana (thale cress)
ORGANISM
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1
De Veylder, L., Beeckman, T., Beemster, G. T., Krols, L., Terras, P.,
Landrieu, I., van der Schueren, E., Maes, S., Naudts, M. and Inze, D.
Functional analysis of cyclin-dependent kinase inhibitors of
Arabidopsis
Plant Cell 13 (7), 1653-1668 (2001)
21342510
PUBMED
11449057
2 (bases 1 to 591)
De Veylder, L.
Direct Submission
Submitted (31-OCT-2000) De Veylder L., Departement Plantegenetica,
Vlaams Interuniversitair Instituut voor Biologie (VIB), K.L.
Ledeganckstraat 35, B-9000 Gent, BELGIUM
Location/Qualifiers
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361  AGTCAGTGAAGTGGGGTTTGGGAGAAACGACACAGAAATGGAATCATCATCGGCAACG 420
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456  AAGAGAAACAAACCGGGGTGAGGAAGACTCCACGGCGGGGAGATTGAGGATTTGTTTC 515
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421  AAGAGAAACAAACCGGGGTGAGGAAGACTCCACGGCGGGGAGATTGAGGATTTGTTTC 480
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516  TCGGAGCTAGAGAGTCCAGACGATGAAGAAGCAATTCATAGAAAAGTACAACTTCGAT 575
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576  ATTGTCAATAGCAAGACCGCTTGAAGGTCGCTACAAAGTGGGATCGACTTTAA 626
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541  ATTGTCAATAGCAAGACCGCTTGAAGGTCGCTACAAAGTGGGATCGACTTTAA 591

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VERSION
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  Arabidopsis thaliana (thale cress)
ORGANISM
  Arabidopsis thaliana
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1
Kaneko, T., Katoh, T., Sato, S., Nakamura, A., Asamizu, E. and Tabata, S.
Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC
and BAC clones
DNA Res. 7 (3), 217-221 (2000)
20363099
PUBMED
10907853
2 (bases 1 to 81875)
Kaneko, T., Katoh, T., Sato, S., Nakamura, Y., Asamizu, E. and Tabata, S.
Direct Submission
Submitted (03-SEP-1999) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:yinakamu@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)
Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MW11
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.W. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremli1.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is MHP21 and the 3' clone is MLD14.
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CDS

CDS

CDS

CDS

CDS

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AF208692
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DEFINITION
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(ACK1) gene, promoter region and partial cds.
ACCESSION
AF208692
KEYWORDS
Arabidopsis thaliana (thale cress)
SOURCE
Arabidopsis thaliana
ORGANISM
Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 4116)
Cho,J.W. and Park,S.C.
Cell cycle control study in plant: control of plant growth and
development by G1 specific cyclin D1 and a novel D1 specific cyclin
dependent kinase inhibitor, p22ack1
Unpublished
2 (bases 1 to 4116)
Cho,J.W. and Park,S.C.
Direct Submission
Submitted (28-NOV-1999) Plant Growth and Development, Kumho Life &
Environmental Science Laboratory, 1 Oryongdong Bukku, Kwangju
500-712, Korea
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QY 191 GCGTTTAGCGTCTGATGAATGTTCCG 216
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ATH301558
LOCUS
DEFINITION
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(knp7 gene).
ACCESSION
AJ301558
VERSION
AJ301558.1 GI:14422296
KEYWORDS
cyclin-dependent kinase inhibitor; knp7 gene.
SOURCE
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ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1

AUTHORS De Veylder, L., Beekman, T., Beemster, G.T., Krols, L., Terras, P., Landrieu, I., van der Schueren, E., Maes, S., Naudts, M. and Inze, D.
TITLE Functional analysis of cyclin-dependent kinase inhibitors of Arabidopsis
JOURNAL Plant Cell 13 (7), 1653-1668 (2001)
MEDLINE 21342510
PubMed 11449057
REFERENCE 2 (bases 1 to 588)
AUTHORS de Veylder, L.
TITLE Direct Submission
JOURNAL Submitted (31-OCT-2000) De Veylder L., Departement Plantegenetica, Vlaams Interuniversitair Instituut voor Biologie (VIB), K.L.
Ledegeankstraat 35, B-9000 Gent, BELGIUM
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QY 224 CGGTGGAGAGAAAGTGATCA---GTCTCGAGTATCAGCTCGCGTTGTTTCCACAGTGA 280
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Db 579 GAAA 582
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LOCUS AX008798 642 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 8 from Patent WO9964599.
ACCESSION AX008798
VERSION AX008798.1 GI:9996262
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE
1
AUTHORS Fowke, L.C., Wang, H. and Crosby, W.L.
TITLE Cyclin-dependent kinase inhibitors as plant growth regulators
JOURNAL Patent: WO 9964599-A 8 16-DEC-1999;
FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD
(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV
SASKATCHEWAN TECHNOLOGIES (CA)
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VERSION	AX463067.1		
GI	21886080		
KEYWORDS			
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
REFERENCE	1 Arabidopsis thaliana (thale cress)		
AUTHORS	Powke,L.C., Wang H. and Zhou,Y.		
TITLE	Modulation of plant cyclin-dependent kinase inhibitor activity		
JOURNAL	Patent: WO 0250292-A 8 27-JUN-2002;		
	University of Saskatchewan Technologies (CA); Minister of		
	Agriculture and Agrifood Canada (CA)		
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Best Local Similarity	63.0%; Pred.No. 1e-23;		
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Db	501	TGATGACTTTTTCTCGGGCGGAGAG-----ATCGAACAGAAACGATTCACAGAAA	554
Qy	563	GTACAACTTCGATATTGTTCATGACGAACCGCTTGAAGGTCGGTTACAAGTGGGATCGACT	622
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Qy	623	TTAA	626
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DEFINITION	I66494		
ACCESSION	166494		
VERSION	166494.1		
KEYWORDS	GI:2724471		
SOURCE	Unknown.		
ORGANISM	Unknown.		
	Unclassified.		

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Best Local Similarity 66.9%; Pred. No. 0.00078;
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QY 600 GCTCGCTACAAGTGGGATC 618
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Db 597 GGACGCTACGAGTGGGTTT 615

RESULT 13
AY439102 597 bp mRNA linear PLN 01-MAY-2004
LOCUS Glycine max cyclin-dependent kinase inhibitor 1;2 mRNA, complete
DEFINITION cds.
ACCESSION AY439102 GI:46844157
VERSION AY439102.1
KEYWORDS Glycine max (soybean)
SOURCE Glycine max
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
1 (bases 1 to 597)
Li, S., Reverdatto, S. and Nielsen, N.C.
cDNA of cell-cycle genes in soybean cotyledons
UNPUBLISHED
2 (bases 1 to 597)
Li, S., Reverdatto, S. and Nielsen, N.C.
Direct Submission
Submitted (16-OCT-2003) ARS-USDA, Agronomy, Purdue University, 1150
Lilly Hall of Life Sciences, West Lafayette, IN 47906-1150, USA
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CDS
1..597
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ORIGIN
Query Match 7.9%; Score 49.6; DB 8; Length 597;
Best Local Similarity 72.7%; Pred. No. 0.0074;
Matches 64; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 535 ACGATAAGAAGCAATTCATAGAAAAGTACAACCTTCGATATTGTCAATGACGAAACCGC 594
|||||
Db 521 AAGACATTCAGAACGATTTCAAGACAGATACATATGATATTGTGAAGGACGTACCGC 580
|||||

QY 595 TTGAAGGTCGCTACAAAGTGGGATCGACT 622
|||||
Db 560 TGAAGAGGACGCTACGAGTGGGTTCAATT 587
|||||

RESULT 14
AY439101 618 bp mRNA linear PLN 01-MAY-2004
LOCUS Glycine max cyclin-dependent kinase inhibitor 1;1 mRNA, complete
DEFINITION cds.
ACCESSION AY439101 GI:42362357
VERSION AY439101.1
KEYWORDS Glycine max (soybean)
SOURCE Glycine max
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
1 (bases 1 to 618)
Li, S., Reverdatto, S. and Nielsen, N.C.
cDNA of cell-cycle genes in soybean cotyledons
UNPUBLISHED
2 (bases 1 to 618)
Li, S., Reverdatto, S. and Nielsen, N.C.
Direct Submission
Submitted (16-OCT-2003) ARS-USDA, Agronomy, Purdue University, 1150
Lilly Hall of Life Sciences, West Lafayette, IN 47906-1150, USA
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Location/Qualifiers
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ORIGIN
Query Match 7.5%; Score 47.2; DB 8; Length 618;
Best Local Similarity 72.6%; Pred. No. 0.036;
Matches 61; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

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Db 521 AAGACATTCAGAACGATTTCAAGACAGATACATATGATATTGTGAAGGACGTACCGC 580
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QY 595 TTGAAGGTCGCTACAAAGTGGGATC 618
|||||
Db 581 TGAAGAGGACGCTACGAGTGGGTTT 604
|||||

RESULT 15
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LOCUS Arabidopsis thaliana chromosome I BAC F14J22 genomic sequence,
DEFINITION complete sequence.
ACCESSION AC011807 GI:6693374
VERSION AC011807.4
KEYWORDS HTG.
SOURCE Arabidopsis thaliana (chale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.

```


REFERENCE AUTHORS	1 (bases 1 to 104679) Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V.S., Walker,M., Yu.G., Ecker,J., Theologis,A. and Davis,R.W. Unpublished
JOURNAL REFERENCE AUTHORS	2 (bases 1 to 104679) Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Nguyen,M., Lam,B., Southwick,A., Bei,Q., Buehler,E., Chin,C., Chiodi,J., Choi,E., Dunn,P., Gonzalez,A., Howng,B., Kim,C., Koo,T., Lee,J.M., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S., Mukharasy,N., Phan,P., Sakano,H., Schwartz,J., Shinn,P., Thaveri,A., Toriumi,M., Vaysberg,M., Walker,M., Yu.G., Ecker,J., Theologis,A. and Davis,R.W. Direct Submission
TITLE JOURNAL	Direct Submission Submitted (15-OCT-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
REFERENCE AUTHORS	3 (bases 1 to 104679) Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V., Walker,M., Yu.G., Ecker,J., Theologis,A. and Davis,R.W. Direct Submission
TITLE JOURNAL	Direct Submission Submitted (14-JAN-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
REFERENCE AUTHORS	4 (bases 1 to 104679) Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A. and Davis,R.W. Direct Submission
TITLE JOURNAL	Direct Submission Submitted (13-SEP-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
COMMENT	On Jan 14, 2000 this sequence version replaced gi:6692246. Bases 92948-104679 of IGF clone F14J22 overlap with bases 1-11732 of IGF clone F13P21 (gb AC007504). e-mail for correspondence: arabesque@stanford.edu Genes with similarity to proteins in the databases are named 'putative', '-like' or 'similar to'. Genes that have EST similarity but no significant protein similarity are described as 'unknown proteins'. Genes that are annotated based only on gene prediction software are described as 'hypothetical proteins'. The gene prediction programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://combio.ornl.gov/section/index.html), GENSCAN (Chris Burge, http://genes.mit.edu/GENSCAN.), FEXA (Victor Solovyev, http://genomic.sanger.ac.uk/gf/gf.shtml), and NetPlantGene (S.M. Hebagaard, et al., CBS Technical University of Denmark,http://www.cbs.dtu.dk/NetPlantGene.html). Location/Qualifiers 1. .104679 /organism="Arabidopsis thaliana" /mol_type="genomic DNA" /db_xref="taxon:3702" /chromosomes="1" /clone="F14J22" 6567. .7832 /gene="F14J22.1" 6567. .7832 /gene="F14J22.1" /codon_start=1 /product="Hypothetical protein" /protein_id="AAG13057.1" /db_xref="GI:10120432" /translation="MPGNLEPLDGIQIPYHFRCPISLDLMSDPVTISTGOTYDRTSI DSWIANGNTCPVTFVALSDFTLIPNHTLRLIQWCVNRSNGVERIPTEKQADPI SVRLLSASAITGTHSVRSRAAIRRLGLARDEKRVLLIAGHNAREILVRILFA DIETTSLSVESLALLVLLHMTETECEAVASDPFRGFWMTLLLPDSSIEIRVNAA ALIEMVLTKAASMDLKLIIISGSDSIFEGVLDDLKNPISRRALKIGIKAIKALCLVKQ
FEATURES source	TRHLAISAGAPGILIDRLAADFDRCDTERGLATVELLCRLPEGCAAFGEHALTVPLMV XTILRVSDRATEYAGALLALCTAERCRCDEAAAAGLVTLQLLLLVQSDCTERAKKAQ MLLLLRDSWDDSTVHSDDDPNRSEVAF" complement (10438. .12278) /gene="F14J22.2" complement (join(10438. .11034,11973. .12278)) /gene="F14J22.2" /codon_start=1 /evidence=not_experimental /product="Hypothetical protein" /protein_id="AAG13058.1" /db_xref="GI:10120433" /translation="MTNAQLGQGFWMGISNDDSGGCKRIEKLPLSPHSHPSP IQTTVTKGKRTKRNKNDKHEESPDEHIIHWTERRERKMRDMFSLKHLALLPOLPPK ADKSTIDEAVSSIKSLEOTLKLEMQKLEKLOYSSASTNTPTTTPAYASSSSSPT ALLTPISNHPIDATIDSYPRAAFADQVSSSSAAAANLPYCNDPIVNFDTWSSRNV VLTIKGNBAFFNLCVPKHKPGVFTSCVLYLFKYNNEVLFAVNSNVFVSTVIQAVS YTYNHFYHMCIGDIYILPWFPPFM" complement (17103. .20116) /gene="F14J22.3" complement (join(17103. .17345,17435. .17638,17727. .17921, 17999. .18133,18225. .18314,18416. .18493,18579. .19235, 19372. .19490,19822. .20116)) /gene="F14J22.3" /codon_start=1 /evidence=not_experimental /product="Putative Poly-A Binding Protein" /protein_id="AAG13056.1" /db_xref="GI:10120431" /translation="MAQIQHQGNANGVAVPGAAAAFAAAAAAGAAAAAGAAQOQT TSLYVGLDLDATVDSQLPEAFQAGQVSVVRCRDMTTRSLGIVGVNYATPDQASRA LNEINFALNGRAIRVMYSVRDPSLRKSGVGNIFIKLNDKSIDKALHETSAFGPIL SCKVADPSGQSKGYFQVQDTEAQAQIDKLGMLLNDKQVYVGPVHKLQRPDSG EKVFTNIVYVKNLSSELSDELNKVGFEGVTTCVIMRDGEGSKGFGVNFENSD AARVADALNGKTFDDKEMFVKAQKSERETTELKQKFEKSLKAAKSKQSNLYVKNL DESVTDKLREHFAFGTITTSCKVMRDPGVSRSRGVFAFSTPEEATRAITEMGKMI VTKPLYVALAQRKDRKARLQAFQSMRPNMPPAVGMOMYPPGPPMGQQLFYQG GPPAMI PQGFGYQQLVPGMRPGSGPMPNPFMPMQOQQOQQOQQOQQOQQOQQOQQO ALPOQPSPMNOQQMHPRGEMVRYRQDYNVTMEGPTQNMLSVRYDYSVSGGVHRRG PTSQPFVIALATRIANAAPQQQTMLEGNLYPLVEQLEPESAAKVTGMLLEMDQTEV LHLLSEPEALKAKVTEAMDVLRSVAQQQAAGADQLASLSLGDNIVP" 24077. .25793 /gene="F14J22.4" join(24077. .24984,25103. .25793) /gene="F14J22.4" /evidence=not_experimental /note="Unknown protein" /codon_start=1 /evidence=not_experimental /protein_id="AAG13059.1" /db_xref="GI:10120434" /translation="MASILSILLILSLNSLHFTSTTGNHINDRKLSLEIILGGNDN NPPSPSPPEPEPADCPDPDPDPDPDPDPDPDPDPDPDPDPDPDPDPDPDPDPDP PAPPKQSPPTDLPLFASLLKKVYVLRQFADADKLKSWEGPDICNKLGLCK AIPKTKHALASVQENLGRKIGIKLIDNFDLKEVTI PHANSNGFTGSPVDF SNKLXYELDLNNKLTGDPTSVLKGNNLTFLDRFNSFGSGVPPQVFNLDLVLFI NNNLVKRLPLNLGSI TALYITFANNRFTGPISIGNIKYQLQVLEVLNNKLTGLCPY QIGNLTRATVDFGNQLTGPIPYSGCLETMEQLNAGNKFYGTIPEIVCEIACLQN VLSNNYFTQVGPCKRLIKKIMDSVMNCILDLPNQKTPSECAKFFMRKQTCPSKS LFTVPCDNPNRGKPDQERLEEKAAQVSHPTYNTLNPDLRLNL" complement (27081. .29147) /gene="F14J22.5" complement (join(27081. .27408,27492. .27578,27658. .27881, 27973. .28276,28385. .28483,28564. .28824,29045. .29147)) /gene="F14J22.5" complement (join(27388. .27408,27492. .27578,27658. .27881, 27973. .28276,28385. .28483,28564. .28824,29045. .29138)) /gene="F14J22.5" /note="Unknown protein" /codon_start=1 /evidence=not_experimental

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 30, 2005, 09:05:47 ; Search time 476 Seconds
(without alignments)
7785.206 Million cell updates/sec

Title: US-09-980-758A-7
Perfect score: 626
Sequence: 1 ctgagattaccacaaat.....acaagtgagtgactttaaa 626

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:.*
1: Geneseqn1980s:.*
2: Geneseqn1990s:.*
3: Geneseqn2000s:.*
4: Geneseqn2001as:.*
5: Geneseqn2001bs:.*
6: Geneseqn2002as:.*
7: Geneseqn2002bs:.*
8: Geneseqn2003as:.*
9: Geneseqn2003bs:.*
10: Geneseqn2003cs:.*
11: Geneseqn2003ds:.*
12: Geneseqn2004as:.*
13: Geneseqn2004bs:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	626	100.0	626	5 AAC85201	AAC85201 Plant D-1
2	612.8	97.9	824	3 AAZ29417	Aaz29417 Arabidops
3	612.8	97.9	824	6 AAD40765	Aad40765 Arabidops
4	122	19.5	642	3 AAZ29418	Aaz29418 Arabidops
5	122	19.5	642	6 AAD40766	Aad40766 Arabidops
6	52	8.3	467	3 AAA95291	Aaa95291 Soybean c
7	48.8	7.8	424	3 AAN02392	Aan02392 Soybean c
8	48.8	7.8	424	3 AAA95278	Aaa95278 Soybean c
9	48.8	7.8	620	3 AAA95287	Aaa95287 Soybean c
10	48.8	7.8	620	3 AAN02401	Aan02401 Cyclin de
11	47.2	7.5	1116	3 AAN02402	Aan02402 Cyclin de
12	47.2	7.5	1116	3 AAA95288	Aaa95288 Soybean c
13	46.2	7.4	804	3 AAZ29420	Aaz29420 Chenopodi
14	46.2	7.4	804	6 AAD40768	Aad40768 Chenopodi
15	45.8	7.3	377	6 AAD40762	Aad40762 Arabidops
16	45.8	7.3	443	6 AAD40763	Aad40763 Arabidops
17	45.8	7.3	779	3 AAC47352	Aac47352 Arabidops
18	45.8	7.3	780	3 AAC36958	Aac36958 Arabidops
19	45.8	7.3	904	3 AAC29415	Aac29415 Arabidops
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C	21	45.8	7.3	1022	6	ABN98442	Abn98442 Arabidops
	22	44.6	7.1	870	3	AAA95293	Aaa95293 Arabidops
	23	44.6	7.1	870	3	AAC46465	Aac46465 Arabidops
	24	44.6	7.1	870	12	ADN72346	Adn72346 Thale cre
	25	44.6	7.1	1290	6	AAD40769	Aad40769 Arabidops
	26	44.6	7.1	1341	3	AAC33295	Aac33295 Arabidops
	27	44	7.0	470	3	AAN02403	Aan02403 Cyclin de
	28	44	7.0	470	3	AAA95289	Aaa95289 Soybean c
	29	43	6.9	533	3	AAD29419	Aad29419 Arabidops
	30	43	6.9	533	6	AAD40767	Aad40767 Arabidops
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	32	43	6.9	797	6	AAD40771	Aad40771 Arabidops
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	35	41	6.5	2000	8	ADA71938	Ada71938 Rice gene
	36	40.8	6.5	1193	2	AAK25017	Aak25017 Alfalfa c
	37	39.2	6.3	528	10	ACC60133	Acc60133 Rice endo
	38	38.8	6.2	2355	13	ADS49209	Ads49209 Bacterial
	39	38.2	6.1	3143	2	AAT59504	Aat59504 Candida a
	40	38.2	6.1	3224	2	AAT66688	Aat66688 Candida a
	41	38	6.1	571	5	AAS90731	Aas90731 DNA encod
	42	38	6.1	906	5	AAS88069	Aas88069 DNA encod
	43	38	6.1	906	5	AAS68116	Aas68116 DNA encod
	44	38	6.1	993	5	AAS90706	Aas90706 DNA encod
	45	38	6.1	993	5	AAS68118	Aas68118 DNA encod

ALIGNMENTS

RESULT 1
AAC85201
ID AAC85201 standard; DNA; 626 BP.
XX
AC AAC85201;
XX
DT 22-MAR-2001 (first entry)
XX
DE Plant D-like cyclin inhibitor BRO4 coding sequence.
XX
KW Plant; D-like cyclin inhibitor gene; BRO4; hyperplastic; variant;
KW growth rate; dividing cells; inactivation; protoplast; seed; root cell;
KW meristem; leaf; ss.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
CDS 36..626
FT /*tag= a
FT /product= "BRO4"
XX
XX WO200069883-A1.
XX
PD 23-NOV-2000.
XX
PF 15-MAY-2000; 2000WO-US013379.
XX
PR 14-MAY-1999; 99US-0134373P.
XX
PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.
XX
PI Roberts J, Kelly B;
XX
DR WPI; 2001-024998/03.
XX
P-PSDB; AAB47001.
XX
PT Functionally inactivating expression of plant D-like cyclin inhibitor
PT gene for producing a hyperplastic variant plant, modulating the growth
PT and/or yield of plants, and increasing the proportion of dividing cells.
PS Claim 16; Page 41; 50pp; English.
XX
CC The sequence given in AAC85201 represents a plant D-like cyclin inhibitor

CC gene, BRO4. This sequence may be used to produce a hyperplastic variant
 CC plant, increase the growth rate of a plant, or increase the proportion of
 CC dividing cells in a plant cell population, relative to a wild-type plant,
 CC by functionally inactivating the expression of a plant D-like cyclin
 CC inhibitor gene in a plant. This sequence is homologous to a sequence
 CC present in a D-like cyclin inhibitor gene and when integrated at the
 CC corresponding locus, functionally inactivates plant D-like cyclin
 CC inhibitor protein expression. BRO4 is useful for producing hyperplastic
 CC variant plants, increasing the growth rate of a plant and for increasing
 CC the proportion of dividing cells in a plant cell population comprising
 CC protoplast, seeds, root cells, meristem cells or leaf cells
 XX
 SQ Sequence 626 BP; 202 A; 131 C; 156 G; 137 T; 0 U; 0 Other;

Query Match 100.0%; Score 626; DB 5; Length 626;
 Best Local Similarity 100.0%; Pred. No. 2.7e-183;
 Matches 626; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 1 CTCGAGATTACCCAAAATCCAGAGAGAAAAAATGAGCGAGAGAAAGCGAGAGCTTG 60
 QY 61 CAGAGAGAGCTTCAGACAGAGCTTCTCACCACCTGAAGAAAACGAGCTTAATGATCTT 120
 Db 61 CAGAGAGAGCTTTCAGACAGAGCTTCTCACCACCTGAAGAAAACGAGCTTAATGATCTT 120
 QY 121 CTGATTATCATCCGGACTCTCATGAGCTCATGCTTCGCGGTTTCATCTTCTCCGTTG 180
 Db 121 CTGATTATCATCCGGACTCTCATGAGCTCATGCTTCGCGGTTTCATCTTCTCCGTTG 180
 QY 181 CTTGCTCGCGGCTTTAGCGTCTGATGAATGTTCCGTTACCATCGGTGGAGAAAGTG 240
 Db 181 CTTGCTCGCGGCTTTAGCGTCTGATGAATGTTCCGTTACCATCGGTGGAGAAAGTG 240
 QY 241 ATCAGTCTCCAGATCAGCTCCGTTGTTTCCAGAGTGAATCGAAGAAATCGGAGAGA 300
 Db 241 ATCAGTCTCCAGATCAGCTCCGTTGTTTCCAGAGTGAATCGAAGAAATCGGAGAGA 300
 QY 301 ACAGTTCTGCTGTTGGTGTAGATCTGGAGGATCATCAATCGAAACCGAAACCGAACT 360
 Db 301 ACAGTTCTGCTGTTGGTGTAGATCTGGAGGATCATCAATCGAAACCGAAACCGAACT 360
 QY 361 CAACATTATCACCAGCAATTTTCAGAAAAGAGAGAGTCCAGTGAGGAGGTTTGGAG 420
 Db 361 CAACATTATCACCAGCAATTTTCAGAAAAGAGAGAGTCCAGTGAGTGGAGGTTTGGAG 420
 QY 421 AAACGACAAAGAAATGGAATCATCATCGGCAACGAGAGAAACCAACCGGGGTGAGGA 480
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 QY 481 AGACTCCAAACCGCGGAGATTGAGGATTTGTTCTCGAGCTAGAGAGTCCAGACGATA 540
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 QY 541 AGAAGAGCAATTCATAGAAAAGTACAACTTCGATATTGTCAATGACGAAACCGTTGAAG 600
 Db 541 AGAAGAGCAATTCATAGAAAAGTACAACTTCGATATTGTCAATGACGAAACCGTTGAAG 600
 QY 601 GTCGCTACAAGTGGGATCGACTTTAA 626
 Db 601 GTCGCTACAAGTGGGATCGACTTTAA 626

RESULT 2
 AAZ29417
 ID AAZ29417 standard; cDNA; 824 BP.
 XX
 AC AAZ29417;
 XX
 XX 29-FEB-2000 (first entry)
 XX
 DE Arabidopsis thaliana CDK inhibitor, ICN2 encoding cDNA.
 XX

KW Cyclin-Dependent kinase inhibitor; CDK; Interactor of Cyclin 2; ICN2;
 KW Cdc2a; D-class cyclin; CycD1; CycD2; CycD3; morphogenesis;
 KW antisense construct; tissue-specific promoter; transgenic plant;
 KW male sterility; ds.
 XX Unidentified.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 1..639
 FT /*tag= a
 FT /product= "ICN2"
 XX
 PN W09964599-A1.
 XX
 PD 16-DEC-1999.
 XX
 PF 08-JUN-1999; 99WO-CA000532.
 XX
 PR 08-JUN-1999; 98CA-02235978.
 PR 31-DEC-1998; 98CA-02256121.
 XX
 PA (MIAC) AGRIC & AGRIFOOD CANADA.
 PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
 PA (CANA) NAT RES COUNCIL CANADA.
 XX
 PI Wang H, Fowke LC, Crosby WL;
 XX
 XX WPI: 2000-097540/08.
 DR P-PSDB; AAY44337.
 XX
 PT Modifying plant cell development using nucleic acid encoding inhibitor of
 PT cyclin-dependent kinase, or corresponding antisense sequence, e.g. for
 PT inducing male sterility.
 XX
 XX Disclosure; Fig 4; 58pp; English.
 PS
 XX
 CC The present sequence is a cDNA encoding ICN2 which inhibits A. thaliana
 CC Cyclin-Dependent kinase (CDK). Interactor of Cyclin 2 (ICN2) interacts
 CC with Cdc2a, D-class cyclins, CycD1, CycD2 and CycD3 and shares functional
 CC and sequence similarity with IKK1 growth, morphogenesis, multiplication,
 CC enlargement, differentiation and maturation of plant cells can be
 CC modified by transforming them with nucleic acid encoding CDK inhibitor or
 CC antisense construct complementary to the inhibitor gene, operably linked
 CC to a tissue-specific promoter. The transgenic plants exhibit alteration
 CC of traits such as petals, male sterility and ability to set seeds
 XX
 SQ Sequence 824 BP; 287 A; 164 C; 185 G; 188 T; 0 U; 0 Other;

Query Match 97.9%; Score 612.8; DB 3; Length 824;
 Best Local Similarity 99.7%; Pred. No. 3.8e-179;
 Matches 614; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 11 ACCCAAAAATCCAGAGAGAAAAAATGAGCGAGAGAAAGCGAGAGCTTGCGAGAGAGC 70
 Db 24 ACACAAAATCCAGAGAGAAAAAATGAGCGAGAGAAAGCGAGAGCTTGCGAGAGAGC 83
 QY 71 TTCAAGCACAAGCTTCTCACCACCTGAAGAAAACGAAAGCTTAATGATCTTCTGATTCTATC 130
 Db 84 TTCAAGCACAAGCTTCTCACCACCTGAAGAAAACGAAAGCTTAATGATCTTCTGATTCTATC 143
 QY 131 ACGGACTCTCATGACGTCATCGTCTTCGCGGTTTCATCTTCTTCGTTGTTCTTCGTCGCGC 190
 Db 144 ACGGACTCTCATGACGTCATCGTCTTCGCGGTTTCATCTTCTTCGTTGTTCTTCGTCGCGC 203
 QY 191 GGCTTTAGCGTCTCATGATGAATGTTCCGTTTACCATCGGTGGAGAAAGTGTATGATCTCTC 250
 Db 204 GGCTTTAGCGTCTCATGATGAATGTTCCGTTTACCATCGGTGGAGAAAGTGTATGATCTCTC 263
 QY 251 GAGTATCAGTCTCCGTTGTTTCCAGCTGAATCGAAGAAATCGCGAAGAACAGTTCGTC 310
 Db 264 GAGTATCAGTCTCCGTTGTTTCCAGCTGAATCGAAGAAATCGCGAAGAACAGTTCGTC 323
 QY 311 GTTTGGTGTAGATCTGGAGGATCATCAATCGAAACCGAAACCGAAACCTCAACATTCAT 370

KW Cdc2a; D-class cyclin; CycD1; CycD2; CycD3; morphogenesis;
 KW antisense construct; tissue-specific promoter; transgenic plant;
 KW male sterility; ds.

OS Unidentified.

XX Key Location/Qualifiers
 FH 1..624
 FT /*tag= a
 FT /product= "ICN6"

XX WO9964599-A1.

XX 16-DEC-1999.

XX 08-JUN-1999; 99WO-CA000532.

XX 08-JUN-1998; 98CA-02235978.

XX 31-DEC-1998; 98CA-02256121.

XX (MIAC) AGRIC & AGRIFOOD CANADA.

PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.

PA (CANA) NAT RES COUNCIL CANADA.

PI Wang H, Fowke LC, Crosby WL;

XX WPI; 2000-097540/08.
 DR P-PSDB; AAY44338.

XX Modifying plant cell development using nucleic acid encoding inhibitor of
 PT cyclin-dependent kinase, or corresponding antisense sequence, e.g. for
 PT inducing male sterility.

XX Disclosure; Fig 5; 58pp; English.

XX The present sequence is a cDNA encoding ICN6 which inhibits A. thaliana
 CC Cyclin-Dependent kinase (CDK). Interactor of Cyclin 6 (ICN6) interacts
 CC with Cdc2a, D-class cyclins, CycD1, CycD2 and CycD3 and shares functional
 CC and sequence similarity with ICK1. Growth, morphogenesis, multiplication,
 CC enlargement, differentiation and maturation of plant cells can be
 CC modified by transforming them with nucleic acid encoding CDK inhibitor or
 CC antisense construct complementary to the inhibitor gene, operably linked
 CC to a tissue-specific promoter. The transgenic plants exhibit alteration
 CC of traits such as petals, male sterility and ability to set seeds

XX Sequence 642 BP; 211 A; 140 C; 152 G; 139 T; 0 U; 0 Other;

Query Match 19.5%; Score 122; DB 3; Length 642;

Best Local Similarity 63.0%; Pred. No. 5.3e-27;

Matches 305; Conservative 0; Mismatches 140; Indels 39; Gaps 6;

QY 164 TTCATCTTCTCCGTTGCTTCTCGCGCGCTTTAGCGTCTGATGAATGTTCCGTTACCAT 223

DB 153 TTCTCTTTCTTCTCTGCTTACTCGGTTTCAGATTCGCGAGGTTTCTCTCGTCCGCTT 212

QY 224 CGGTGGAGAGAAAGTATCA---GTCCTCAGATATCAGCTCGGTTGTTTCCACAGTGA 280

DB 213 ATCTGAAGAGAGACGATCATCTAAGCTCAGCATCAGCTCTGTTGTTCCAGCAGCA 272

QY 281 ATCGAAAGAAATTCGGAAGAACAGTTCCTGTTGGTGTAGATCTGGAGGATCATCAAT 340

DB 273 AACTAACGAAATCGTACTCGTCTTCCATTTTC-----AGATCTGGAGGCTCATGAAT 326

QY 341 CGAAACCGAAACCGAAATTCACATTCACACGAGCAATTCAGAAAGACGAGTCC 400

DB 327 CT---CCGAAACCGAAATTCACGTTTACTCACCAACAAATTCAGAAACACGGGAATTC 383

QY 401 AGTGAGTGAGGTTTGGGAGAAACGACACAGAAATGGAATCATCATCGCAACGAGAG 460

DB 384 ATCAAGCGAGAAATCTGGAGAA---ACAGCAGAAATGCACTCGGCGACGCGGAGATGAG 440

QY 461 AAAACAAACCGGGGTGTAGAGAA-----CTCCAAACGCGCGCGGAGAT 502

Db 441 AGATCAGAGAAAGACGGAGAAAGAGAGAGATCGAAATAATCACCGACGCGCAGAGCT 500

QY 503 TGAGGATTTGTTCTCGGAGCTAGAGAGTCCAGACGATAGAGAGCAATTCATAGAAAA 562

Db 501 TGATGACTTTTTCGCGCGCGGAGAG-----ATACGAAACAGAAACCGATTCACAGAAA 554

QY 563 GTACAACCTTCGATATTGTCAATGACGAACCGCTTGAAGGTCGCTTACAAAGTGGGATCGACT 622

Db 555 GTACAACCTTACGACATCGTCAATGATACGCCGCTTGAAGGTCGCTTACCAAGTGGGTTAGTCT 614

QY 623 TTAA 626

Db 615 GAAA 618

RESULT 5

AAD40766

ID AAD40766 standard; cDNA; 642 BP.

XX AAD40766;

XX 30-OCT-2002 (first entry)

XX Arabidopsis thaliana ICN6 cDNA.

XX Plant development; cyclin-dependent kinase; CDK inhibitor; ICK1; ICK2;

XX ICN2; ICN6; ICN7; ICN8; ICNK; morphogenesis; maturation; enlargement;

XX plant breeding; growth; gene; ss.

XX Arabidopsis thaliana.

XX Key Location/Qualifiers

FT 1..624

FT /*tag= a "ICN6 protein #1"

FT /note= "No start codon"

FT /partial

FT CDS 37..624

FT /*tag= b

FT /product= "ICN6 protein #2"

XX WO200250292-A2.

XX 27-JUN-2002.

XX 18-DEC-2001; 2001WO-CA001825.

XX 18-DEC-2000; 2000US-0255908P.

XX (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.

XX (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.

XX Wang H, Zhou Y, Fowke LC;

XX WPI; 2002-519888/55.

DR P-PSDB; AAE25105, AAE25106.

XX Modifying plant development, e.g. growth or maturation, which is

XX particularly useful in plant breeding, by introducing nucleic acids

XX coding for cyclin-dependent kinase (CDK) inhibitor, cyclin or proteins

XX that bind to CDK inhibitors.

XX Disclosure; Fig 5; 89pp; English.

XX The invention relates to a method for the development of a plant. The

XX method involves introducing into a plant cell a nucleic acid encoding a

XX protein that binds or interacts with a cyclin-dependent kinase (CDK)

XX inhibitor polypeptide (such as ICK1, ICK2, ICN2, ICN6, ICN7, ICN8 and

XX ICKK), a cyclin polypeptide, a CDK, or a polypeptide that modulates the

XX degradation of a CDK inhibitor polypeptide. The method is useful for

XX modifying the growth and development of plants e.g. morphogenesis,

XX growth, multiplication, enlargement, differentiation or maturation of a

XX cell or plant. It is particularly useful in plant breeding. The present

```

CC sequence is A. thaliana ICN6 cDNA
XX
SQ Sequence 642 BP; 211 A; 140 C; 152 G; 139 T; 0 U; 0 Other;

Query Match      19.5%; Score 122; DB 6; Length 642;
Best Local Similarity 63.0%; Pred. No. 5.3e-27;
Matches 305; Conservative 0; Mismatches 140; Indels 39; Gaps 6;

QY 164 TTTCATCTTCTTCGGTTCGTCGGGGGTTAGGCTGATGAATGTTCCGTTACCAT 223
DB 153 TTTCCTCTTCTCTCGCTTACTCGGTTTCAGATTCCGGAGGTTTCTGCTCCGTCGTT 212
QY 224 CGGTGCAGAGAAGATGATCA---GTCTCGAGTATCAGTCGCGTTGTTTACCAAGTCA 280
DB 213 ATCTGAAGAAGAAGACGATCATCTAAGCTCAAGCATCAGCTCTGGTTGTTCCAGCGCA 272
QY 281 ATCGAAAGAAATCGCGAAGAACAGTTTCGTCGTTTGGTGTAGATCTCGAGGATCATCAAT 340
DB 273 AACTAACGAAATCGCTACTCGTCTTCCATTTTC-----AGATCTGAGGCTCATGAAT 326
QY 341 CGAAACCGAAACCGAAACCTCAACATTCATCACCAGCAATTTTCAGAAAGACGAGTCC 400
DB 327 CT---CCGAAACCGAAATCTCAACGTTACTCACCAACAATTTTCAGGAAACAGGGAATTC 383
QY 401 AGTGAGTGAGGGTTTCGGGAGAACGACAAACAGAAATGGAATCATCATCGSCAACGAGAG 460
DB 384 ATCAAGCGAGAAATCTGGGAGAA---ACAGCAGAAATGGACTCGGACGACGAGATGAG 440
QY 461 AAAACAACCGGGGGTTCGAGGAAGA-----CTCCAACCGCGCGCGAGAT 502
DB 441 AGATCAGAGAAGACGAGGAGAGAGAGAGATGGAAATCACCAGCCGAGGAGCT 500
QY 503 TGAGGATTTGTTCTCGGAGCTAGAGAGTCCAGACGATAGAGAAAGCAATTCATAGAAA 562
DB 501 TGATGACTTTTTCGCGCGCGGAGAG-----ATACGAACAGAAACGATTCACAGAAA 554
QY 563 GTACACTTCGATATGTTCAATGACGAAACGCTTGAGGTCGTTACAGTGGATCGACT 622
DB 555 GTACAACTACGACATCGTCAATGATACGCGGCTTGAAGGTCGGTACCACTGGGTTAGTCT 614
QY 623 TTAA 626
DB 615 GAAA 618

RESULT 6
AAA95291
ID AAA95291 standard; cDNA; 467 BP.
XX
AC AAA95291;
XX
DT 17-JAN-2001 (first entry)
XX
DE Soybean cyclin-dependent kinase inhibitor coding sequence #6.
XX
KW Soybean; cyclin-dependent kinase inhibitor; cell cycle; cell division;
KW CDKI; cell growth; herbicide; ss.
XX
OS Glycine max.
XX
FH Key Location/Qualifiers
FT CDS 29..295
FT /tag= a
FT /product= "CDKI"
FT /partial
XX
PN WO200060087-A2.
XX
PD 12-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US009106.
XX
PR 07-APR-1999; 99US-0128192P.

( DUPO ) DU PONT DE NEMOURS & CO E I.
Klein TW, Weng Z, Cahoon RE;
WPI; 2000-679375/66.
P-PSDB; AAB27257.
Cyclin dependent kinase inhibitor sequences, useful for identifying herbicides and plant growth inhibitors.
Claim 2; Page 52; 58pp; English.
The present sequence is the coding sequence for the soybean cyclin-dependent kinase inhibitor (CDKI). It was isolated by searching a soybean cDNA library for sequences similar to those encoding the CDKI from Chenopodium rubrum, Caenorhabditis elegans and Arabidopsis thaliana. CDKI is involved in the cell cycle, and may promote or inhibit cell division and growth. The coding sequence and the protein it encodes are useful in the production of transgenic plants which produce increased or decreased amounts of the CDKI protein, in the identification of herbicides, in genetic and physical mapping and in the isolation of the CDKI gene in other organisms
SQ Sequence 467 BP; 158 A; 93 C; 95 G; 121 T; 0 U; 0 Other;

Query Match      8.3%; Score 52; DB 3; Length 467;
Best Local Similarity 65.1%; Pred. No. 2.3e-05;
Matches 95; Conservative 0; Mismatches 45; Indels 6; Gaps 1;

QY 477 AGGAGACTCCAAACGCGCGGAGATTGAGGATTTCTTCGGAGCTAGAGATCCAGAC 536
DB 146 AGAAATATTCCAAACGCTTATGAGATGGAGGATTTCTTGTATGCTGAGA-----AG 199
QY 537 GATAAGAGAAGCAATTTCATAGAAAAGTACAACTTCGATATTGTCAATGACGAACCGCTT 596
DB 200 CAGCACAGACAAATTTATGACAGATACATTTTCGACATTTGACATGTCAGTACTCTG 259
QY 597 GAAGTGCTGTACAAAGTGGATCGACT 622
DB 260 CCTGGACGCTACGAGTGGGTCCAGT 285

RESULT 7
AAN02392
ID AAN02392 standard; DNA; 424 BP.
XX
AC AAN02392;
XX
DT 01-NOV-2001 (first entry)
XX
DE Soybean Cyclin dependent kinase inhibitor (CDKI) clone sl2.pk0008.d2.
XX
KW Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; soybean;
KW plant growth inhibitor; ds.
XX
OS Glycine max.
XX
FH Key Location/Qualifiers
FT CDS 2..118
FT /tag= a
FT /product= "CDKI fragment"
FT /partial
FT /note= "No start codon given"
XX
PN WO200060087-A2.
XX
PD 12-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US009106.
XX
PR 07-APR-1999; 99US-0128192P.
XX

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PS Claim 2; Page 49; 58pp; English.

CC The present sequence is the coding sequence for the soybean cyclin-
 CC dependent kinase inhibitor (CDKI). It was isolated by searching a soybean
 CC seedling cDNA library for sequences similar to those encoding the CDKI
 CC from Chenopodium rubrum, Caenorhabditis elegans and Arabidopsis thaliana.
 CC CDKI is involved in the cell cycle, and may promote or inhibit cell
 CC division and growth. The coding sequence and the protein it encodes are
 CC useful in the production of transgenic plants which produce increased or
 CC decreased amounts of the CDKI protein, in the identification of
 CC herbicides, in genetic and physical mapping and in the isolation of the
 CC CDKI gene in other organisms

SQ Sequence 620 BP; 191 A; 111 C; 134 G; 183 T; 0 U; 1 Other;

Query Match 7.8%; Score 48.8; DB 3; Length 620;
 Best Local Similarity 73.8%; Pred. No. 0.00026;
 Matches 62; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 535 ACGATAAGAGAGCAATTCATAGAAAGTACAACTTCGATATTTGTCATATGACGACCGC 594
 DB 167 AGGACATTCAGAAACGATTTCAAGACAGTACAAATTTATGATATTTGTAAGGACGTACCAC 226

QY 595 TTGAAGTGCCTACAGTGGGATC 618
 DB 227 TGGAGGRCGCTACGAGTGGGTTTC 250

RESULT 10

AA02401
 ID AA02401 standard; DNA; 620 BP.

XX AC AA02401;

XX 01-NOV-2001 (first entry)

XX Cyclin dependent kinase inhibitor (CDKI) clone sl2.pk0008.d2.fis.

XX Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; soybean;
 XX plant growth inhibitor; ds.

XX Glycine max.

XX Key Location/Qualifiers
 XX CDS 1..264
 XX /tag= a
 XX /product= "CDKI fragment"
 XX /partial
 XX /note= "No start codon given"

XX WO200060087-A2.

XX 12-OCT-2000.

XX 06-APR-2000; 2000WO-US009106.

XX 07-APR-1999; 99US-0128192P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Klein TM, Weng Z, Cahoon RE;
 XX WPI; 2000-679375/66.
 XX P-PSDB; AAP01951.

XX Cyclin dependent kinase inhibitor sequences, useful for identifying
 XX herbicides and plant growth inhibitors.

XX Claim 2; Page 49; 58pp; English.

XX The invention describes a novel isolated polynucleotide comprising a
 CC nucleotide sequence encoding one of 17 specific cyclin dependent kinase
 CC inhibitor (CDKI) polypeptides, cell cycle regulators involved in control
 CC of cell division, growth and death. The nucleotide sequences can be used
 CC in a vector to transform a host cell to produce the CDKI polypeptide.
 CC They can also be used in methods for selecting and obtaining a nucleic
 CC acid sequence that encodes CDKI or affects the level of CDKI expression.

CC of cell division, growth and death. The nucleotide sequences can be used
 CC in a vector to transform a host cell to produce the CDKI polypeptide.
 CC They can also be used in methods for selecting and obtaining a nucleic
 CC acid sequence that encodes CDKI or affects the level of CDKI expression.

SQ Sequence 620 BP; 191 A; 111 C; 134 G; 183 T; 0 U; 1 Other;

Query Match 7.8%; Score 48.8; DB 3; Length 620;
 Best Local Similarity 73.8%; Pred. No. 0.00026;
 Matches 62; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 535 ACGATAAGAGAGCAATTCATAGAAAGTACAACTTCGATATTTGTCATATGACGACCGC 594
 DB 167 AGGACATTCAGAAACGATTTCAAGACAGTACAAATTTATGATATTTGTAAGGACGTACCAC 226

QY 595 TTGAAGTGCCTACAGTGGGATC 618
 DB 227 TGGAGGRCGCTACGAGTGGGTTTC 250

RESULT 11

AA02402
 ID AA02402 standard; DNA; 1116 BP.

XX AC AA02402;

XX 01-NOV-2001 (first entry)

XX Cyclin dependent kinase inhibitor (CDKI) clone sdp4c.pk025.k23.

XX Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; soybean;
 XX plant growth inhibitor; ds.

XX Glycine max.

XX Key Location/Qualifiers
 XX CDS 143..760
 XX /tag= a
 XX /product= "CDKI"

XX WO200060087-A2.

XX 12-OCT-2000.

XX 06-APR-2000; 2000WO-US009106.

XX 07-APR-1999; 99US-0128192P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Klein TM, Weng Z, Cahoon RE;
 XX WPI; 2000-679375/66.
 XX P-PSDB; AAP01952.

XX Cyclin dependent kinase inhibitor sequences, useful for identifying
 XX herbicides and plant growth inhibitors.

XX Claim 2; Page 49-50; 58pp; English.

XX The invention describes a novel isolated polynucleotide comprising a
 CC nucleotide sequence encoding one of 17 specific cyclin dependent kinase
 CC inhibitor (CDKI) polypeptides, cell cycle regulators involved in control
 CC of cell division, growth and death. The nucleotide sequences can be used
 CC in a vector to transform a host cell to produce the CDKI polypeptide.
 CC They can also be used in methods for selecting and obtaining a nucleic
 CC acid sequence that encodes CDKI or affects the level of CDKI expression.

CC The encoded protein can be used in a method for evaluating a compound for
 CC its ability to inhibit the activity of a CDKI. The inhibitors can be used
 CC as herbicides. They can also be used to inhibit plant growth. The
 CC polynucleotide sequences can be used in gene mapping and as genetic
 CC markers. The sequence encodes the soybean CDKI clone sdp4c.pk025.k23 as
 CC described in the method of the invention

SQ Sequence 1116 BP; 339 A; 236 C; 269 G; 272 T; 0 U; 0 Other;
 Query Match 7.5%; Score 47.2; DB 3; Length 1116;
 Best Local Similarity 72.6%; Pred. No. 0.0011;
 Matches 61; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
 QY 535 ACGATAAGAGCAAGCAATTCATAGAAAAGTACAACTTCGATATTGTCATATGACGAAACCGC 594
 DB 663 AAGACATTCAGAAACGATTTCAAGACAGATACATATGATATTGTTAAGGACGTACCGC 722

QY 595 TTGAAGTCGCTACAAAGTGGGATC 618
 DB 723 TGGAAGGACGCTACGAGTGGGTTT 746

RESULT 12

AAA95288
 ID AAA95288 standard; cDNA; 1116 BP.

AC AAA95288;

DT 17-JAN-2001 (first entry)

DE Soybean cyclin-dependent kinase inhibitor coding sequence #3.

KW Soybean; cyclin-dependent kinase inhibitor; cell cycle; cell division;
 KW CDKI; cell growth; herbicide; ss.

OS Glycine max.

Key Location/Qualifiers
 FH 143..760
 CDS /*tag= a
 FT /product= "CDKI"

PN WO200060087-A2.

PD 12-OCT-2000.

PF 06-APR-2000; 2000WO-US009106.

PR 07-APR-1999; 99US-0128192P.

PA (DUPO) DU PONT DE NEMOURS & CO E I.

PI Klein TM, Weng Z, Cahoon RE;

DR WPI; 2000-679375/66.

DR P-PSDB; AAB27254.

PT Cyclin dependent kinase inhibitor sequences, useful for identifying
 PT herbicides and plant growth inhibitors.

PS Claim 2; Page 49-50; 58pp; English.

CC The present sequence is the coding sequence for the soybean cyclin-
 CC dependent kinase inhibitor (CDKI). It was isolated by searching a soybean
 CC pod cDNA library for sequences similar to those encoding the CDKI from
 CC *Chenopodium rubrum*, *Caenorhabditis elegans* and *Arabidopsis thaliana*. CDKI
 CC is involved in the cell cycle, and may promote or inhibit cell division
 CC and growth. The coding sequence and the protein it encodes are useful in
 CC the production of transgenic plants which produce increased or decreased
 CC amounts of the CDKI protein, in the identification of herbicides, in
 CC genetic and physical mapping and in the isolation of the CDKI gene in
 CC other organisms

SQ Sequence 1116 BP; 339 A; 236 C; 269 G; 272 T; 0 U; 0 Other;
 Query Match 7.5%; Score 47.2; DB 3; Length 1116;
 Best Local Similarity 72.6%; Pred. No. 0.0011;
 Matches 61; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
 QY 535 ACGATAAGAGCAAGCAATTCATAGAAAAGTACAACTTCGATATTGTCATATGACGAAACCGC 594
 DB 663 AAGACATTCAGAAACGATTTCAAGACAGATACATATGATATTGTTAAGGACGTACCGC 722

RESULT 13

AAZ29420
 ID AAZ29420 standard; cDNA; 804 BP.

AC AAZ29420;

DT 29-FEB-2000 (first entry)

DE *Chenopodium rubrum* CDKI1 encoding cDNA.

KW Cyclin-Dependent kinase; CDK; CDKI1; Cdc2a; D-class cyclin; CycD1; CycD2;
 KW CycD3; morphogenesis; transgenic plant; male sterility; ds.

OS *Chenopodium rubrum*.

Key Location/Qualifiers
 FH 58..648
 CDS /*tag= a
 FT /product= "CDKI1"

PN WO9964599-A1.

PD 16-DEC-1999.

PF 08-JUN-1999; 99WO-CA000532.

PR 08-JUN-1998; 98CA-02235978.

PR 31-DEC-1998; 98CA-02256121.

PA (MIAC) AGRIC & AGRIFOOD CANADA.

PA (UYSA) UNIV SASKATCHEWAN TECHNOLOGIES INC.

PA (CANA) NAT RES COUNCIL CANADA.

PI Wang H, Fowke LC, Crosby WL;

WPI; 2000-097540/08.

P-PSDB; AAY44340.

PT Modifying plant cell development using nucleic acid encoding inhibitor of
 PT cyclin-dependent kinase, or corresponding antisense sequence, e.g. for
 PT inducing male sterility.

PS Disclosure; Fig 6; 58pp; English.

CC The present sequence is a cDNA encoding *C. rubrum* CDKI1, which inhibits
 CC *Arabidopsis thaliana* Cyclin-Dependent kinase (CDK). CDKI1 interacts with
 CC Cdc2a, D-class cyclins, CycD1, CycD2 and CycD3 and shares functional and
 CC sequence similarity with ICK1. Growth, morphogenesis, multiplication,
 CC enlargement, differentiation and maturation of plant cells can be
 CC modified by transforming them with *Agrobacterium* strain harbouring an
 CC expression construct of CDKI1. The transgenic plants exhibit alteration
 CC of traits such as petals, male sterility and ability to set seeds

SQ Sequence 804 BP; 254 A; 151 C; 202 G; 197 T; 0 U; 0 Other;

Query Match 7.4%; Score 46.2; DB 3; Length 804;
 Best Local Similarity 59.2%; Pred. No. 0.0019;
 Matches 100; Conservative 0; Mismatches 63; Indels 6; Gaps 1;

Qy	533	AGACGATAAGAAAGCAATTTCATAGAAAAAGTACAACTTCGATATTGTCAATGACGAACC	592
Db	241	ACTC-----AAAGAAAAATTCAGAAGAAGTACAAATTCGATTCGAGAAGGAGAGCC	294
Qy	593	GCTTGAAGTCCGTACAAGTGGG	615
Db	295	ATTAGAGGACGTTACGAATGGG	317

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OM nucleic - nucleic search, using sw model

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(without alignments)
6284.106 Million cell updates/sec

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Perfect score: 626
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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	58	9.3	7218	1	Sequence 14, Appl
C 2	43	6.9	875	4	Sequence 2, Appl
C 3	41.8	6.7	505	4	Sequence 15639, A
C 4	40.8	6.5	1193	4	Sequence 5, Appl
C 5	38.2	6.1	3143	1	Sequence 1, Appl
C 6	38.2	6.1	3143	2	Sequence 1, Appl
C 7	38.2	6.1	3143	5	Sequence 1, Appl
C 8	36.6	5.8	1371	4	Sequence 5113, Ap
C 9	35.6	5.7	738	4	Sequence 1525, Ap
C 10	35.6	5.7	7760	3	Sequence 63, Appl
C 11	35.2	5.6	265	4	Sequence 3165, Ap
C 12	35	5.6	467	4	Sequence 7933, Ap
C 13	35	5.6	467	4	Sequence 23215, A
C 14	35	5.6	954	4	Sequence 608, App
C 15	35	5.6	1104	4	Sequence 686, App
C 16	34.6	5.5	172677	4	Sequence 13444, A
C 17	34.4	5.5	998	3	Sequence 5, Appl
C 18	34	5.4	1837	4	Sequence 4363, Ap
C 19	33.8	5.4	29172	4	Sequence 15520, A
C 20	33.6	5.4	1866	4	Sequence 66, Appl
C 21	33.4	5.3	522	4	Sequence 1015, Ap
C 22	33.4	5.3	522	4	Sequence 2269, Ap
C 23	33.4	5.3	5240	3	Sequence 1400, Ap
C 24	33.4	5.3	2945	4	Sequence 4019, Ap
C 25	33.4	5.3	3123	4	Sequence 3699, Ap
C 26	33.4	5.3	3697	4	Sequence 4317, Ap
C 27	33.4	5.3	3726	4	Sequence 3917, Ap

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ALIGNMENTS

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; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232.463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935.313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: ptzgpt-F1s
US-08-232-463-14

Query Match 9.3%; Score 58; DB 1; Length 7218;

[illegible]

RESULT 2
US 09-526-597D-3
; Sequence 3, Application US/09526597D
; Patent No. 6710227
; GENERAL INFORMATION:
; APPLICANT: De Veylder, Lieven
; APPLICANT: De Almeida, Janice
; APPLICANT: Landrieu, Isabelle
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof

; CURRENT APPLICATION NUMBER: US/09/526,597D

```

; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11)..(658)
US-09-526-597D-3

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	Query Match	6.9%	Score 43;	DB 4;	Length 875;
	Best Local Similarity	69.9%;	Pred. No. 0.0025;		
	Matches	58;	Conservative 0;	Mismatches 25;	Indels 0; Gaps 0;
QY	544	AGAAGCAATTCATAGAAAAGTACAACCTTCGATNTTGTCAATGACGAAACCGCTTTGAAGGTC	603		
Db	573	AGAGGCTATTTCATCGGAGAGTACAACCTTCGACATTGTGAATGATATATCCCCCTCAGCGGAC	632		
QY	604	GCTACAAGTGGGATCGACTTTAA	626		
Db	633	GTTCACGAATGGGTGCACAGTCAAA	655		

RESULT 3
US-09-621-976-15639/C
; Sequence 15639, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

```

? FILE REFERENCE: GENSET.054PR2
? CURRENT APPLICATION NUMBER: US/09/621,976
? CURRENT FILING DATE: 2000-07-21
? NUMBER OF SEQ ID NOS: 19335
? SOFTWARE: Patent.pm
? SEQ ID NO 15639
? LENGTH: 505
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-621-976-15639

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Query Match 6.7%; Score 41.8; DB 4; Length 505;
Best Local Similarity 11.5%; Pred. No. 0.0043;
Matches 36; Conservative 153; Mismatches 120; Indels 4; Gaps 1

296	GAAGAAACAGTTCTGTCGTTTGGTGTAGATCTGGAGGATCATCAAAATCGAAACCGAAACCGA	355
Qy		
338	SMTRKRMMMTYSGMMWTSYKCTKTGKXYTGWKSKKTRWTCTSNRKYMMMSGWARSMKS	279
Db		
356	AACCTCAACATTTCATCACCAGCAATTTACAGAAAGACAGAGTCCTCAGTGAGTGAAGGGTTT	415
Qy		
278	WARSWTSMWAACWCMSSASAYRARRSMYGAARRRMMRAGAGWRRARRRKKRARGKSSMMRKS	219
Db		
416	GGGAGAAAACACACAGAAATGGAATCATCATCGGCAACAGAGAGAAAAACAACCGGGGT	475
Qy		
218	MSSNRMSAGKARCMCRMMMSCRMMSYS CMGSKMCSRGTCAKMRYARYAKRYASSMGKY	159
Db		
476	GAGAGACATCCAAACG---CGGCGGAGATTGAGGATTTGTTCTCGAGAGCTAGAGAGTC	531
Qy		
158	MMGCRWCYAKARMYGYRBSRSTSGRMKYRRRKMYYMKYMMWSWVCVRMGAAMYGM	99
Db		
532	CAGACGATAGAAGAAGCAATTCATAGAAAAGTACAACTTCGATATTGTCAATGACGAAAC	591
Qy		
98	SARAYRWASACKWCSRMMKMMSNMWRCWRSRYRCMMSGKWKYS CCGYCCSACRMC	39
Db		
592	CGGTTGAAGTCG	604
Qy		
38	YCNTRRMKSWSS	26
Db		

RESULT 4
US-09-526-597D-5
; Sequence 5, Application US/09526597D
; Patent No. 6710227
; GENERAL INFORMATION:
; APPLICANT: De Veylder, Lieven
; APPLICANT: De Almeida, Janice
; APPLICANT: Landrieu, Isabelle
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
; FILE REFERENCE: 1187-2

: CURRENT APPLICATION NUMBER: US/09/526.597D

; CURRENT FILING DATE: 2000-03-16

; NUMBER OF SEQ ID NOS: 35

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; SOFTWARE: PatentIn version 3.0

```

; SEQ ID NO 5

```

; LENGTH: 1193
; TYPE: DNA

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TYPE: DNA
ORGANISM: Arabidopsis thaliana

: FEATURE: CREATIVISM: ATTITUDES CHARACTER:

NAME/KEY: CDS

; LOCATION: (92).. (763)

US-09-526-597D-5

Query Match 6.5%; Score 40.8; DB 4; Length 1193;

Best Local Similarity 65.2%; Pred. No. 0.015;
Matches 60; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy	533	AGACGATAAGAAAGCAATTTCATAGAAAAGTACAACTTTCGATATTGTCATAGCAAGACC	592
Db	664	AGCCGAGCAGCAAAAGGAGATTTCATGGAGAAGTACAACTTTCGATCCTGTGACAGAGCAGCC	723

OV 593 GCTTGAAGGTCGCTACAAGTGGGATCGACTTT 624

Db 724 ACTCCAGGCGTTACGAATGGAAAAAGTGT 755

RESULT 5

US-08-485-621-1
; Sequence 1, Application US/08485621
; Patent No. 5691187
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gerhold, David L.
; APPLICANT: Strauss, Allyson Cole
; TITLE OF INVENTION: Anti-fungal Agents and Methods of
; TITLE OF INVENTION: Identifying and Using the Same
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5691187is
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,621
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1584
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3143 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 547..2889
US-08-485-621-1

Query Match 6.1%; Score 38.2; DB 1; Length 3143;
Best Local Similarity 48.8%; Pred. No. 0.18;
Matches 103; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY	328	AGGATCATCAATCGAAACCGAAACCGAAACCTCAACATTCATCACCAGCAATTCAGAA	387
Db	788	AGGAACCTTAAAGTGCCTAAATCCAAATCTACATCTAAAAAGGACACCAAGTTAAGA	847
QY	388	AAGAGACGAGTCCAGTGAGTGGGTTTGGGAGAACGACACAGAAATGGAATCATCAT	447
Db	848	AAGAGAAACTACAGTCAGAGAGGAATCTAAAGCCCAAGCACTAAAGTGAAGAGAAAT	907
QY	448	CGGCAACGAGAGAAAAACACCGGGGGTGGAGGAAGACTCCACGGCGGGAGATTGAGG	507
Db	908	CCAAACTCAATCAGATTCACAGCATCGTTTAAATCTGAACTCTGAAAGAGATCAG	967
QY	508	ATTGTCTCGAGCTAGAGAGTCCAGACGA	538
Db	968	GGTACAAATGGTGGGAAGTGAATCAAGAAGA	998

RESULT 6

US-08-973-831-1

; Sequence 1, Application US/08973831
; Patent No. 5942386
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gerhold, David L.
; APPLICANT: Strauss, Allyson Cole
; TITLE OF INVENTION: Anti-fungal Agents and Methods of
; TITLE OF INVENTION: Identifying and Using the Same
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5942386ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,831
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/485,621
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1584
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3143 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 547..2889
US-08-973-831-1

Query Match 6.1%; Score 38.2; DB 2; Length 3143;
Best Local Similarity 48.8%; Pred. No. 0.18;
Matches 103; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY	328	AGGATCATCAATCGAAACCGAAACCGAAACCTCAACATTCATCACCAGCAATTCAGAA	387
Db	788	AGGAACCTTAAAGTGCCTAAATCCAAATCTACATCTAAAAAGGACACCAAGTTAAGA	847
QY	388	AAGAGACGAGTCCAGTGAGTGGGTTTGGGAGAACGACACAGAAATGGAATCATCAT	447
Db	848	AAGAGAAACTACAGTCAGTCAAGAGGAATCTAAAGCCCAAGCACTAAAGTGAAGAGAAAT	907
QY	448	CGGCAACGAGAGAAAAACACCGGGGGTGGAGGAAGACTCCACGGCGGGAGATTGAGG	507
Db	908	CCAAACTCAATCAGATTCACAGCATCGTTTAAATCTGAACTCTCTGAAAGAGATCAAG	967
QY	508	ATTGTCTCGAGCTAGAGAGTCCAGACGA	538
Db	968	GGTACAAATGGTGGGAAGTGAATCAAGAAGA	998

RESULT 7

PCT-US96-09530A-1

; Sequence 1, Application PC/TUS9609530A
; GENERAL INFORMATION:

```

; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gerhold, David L.
; APPLICANT: Strauss, Allyson Cole
; TITLE OF INVENTION: Anti-fungal Agents and Methods of
; TITLE OF INVENTION: Identifying and Using the Same
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09530A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,621
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,399
; FILING DATE: 21-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1970
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3143 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 547..2889
;
PCT-US96-09530A-1

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; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 5113
; LENGTH: 1371
; TYPE: DNA
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1165)
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unknn
US-09-248-796A-5113

Query Match          5.8%; Score 36.6; DB 4; Length 1371;
Best Local Similarity 48.3%; Pred. No. 0.37;
Matches 102; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

Qy 328 AGGATCATCAAAATCGAAACCGAAACCGAAACCTCAACATTTCATCACCAGCAATTTCAGAA 387
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 443 AGGAACCTAAAAGTCCAGTAATCCAAATCTACATCTTAAAAAGGACACCCAAAGTTAAGA 502

Qy 388 AAGAGACGAGTCCAGTGGAGTGGGTTTGGGAGAAACGACACAGAAATCGAATCATCAT 447
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 503 AAGAGAAAACACTACAGTCAAGAAGAGAAATCTTAAAGGCCACAGCACTTAAAGTGAAGAAGAA 562

Qy 448 CGGCAACGAGAGAGAAAACAAACCGGGGTGAGGAAGACTCCAACGGCGGCGAGATTGAGG 507
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 563 CCAAAACTCAATCAGATTCAACAAGATCGGTTAAATCTGAAACTCTTGAAGAGATCAAG 622

Qy 508 ATTTGTTCTCGAGCTAGAGAGTCCAGACGA 538
Db 623 GGTACAAATGTTGGGAAGTGAATCAAGAAGA 653

RESULT 9
US-09-583-110-1525/c
; Sequence 1525, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 1525
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
; US-09-583-110-1525

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RESULT 8
US-09-248-796A-5113
; Sequence 5113, Application US/09248796A

Db 276 TCATAAAAGTGGATGAACATTTTGGCTCTCTGCAAAATGAGTTTCAATCATTTTC 217
QY 342 GAAACCGAAACCGAAACCTCAACATTCATCACCAGCAATTTTCAGAAAAGAGACGAGTCCA 401
Db 216 CACATAATCAGGTACAACTGACTCATCACCACAGGAATGACTAAAGGGAGACCCGAC 157
QY 402 GTGAGTGAGGGTTTGGGAGAAAGACGACAAAGAAA 435
Db 156 TTGACGAATGATCTCTGCGAATCTACAAGATACA 123

RESULT 10
US-08-961-527-63/c
; Sequence 63, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7760 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-63
Query Match 5.7%; Score 35.6; DB 3; Length 7760;
Best Local Similarity 51.9%; Pred. No. 2.1;
Matches 80; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
QY 282 TCAGAAAGATCGGAGAACAGCTTCGTCGTTTGGTGTAGATCTGAGGATCATCAATTC 341
Db 7588 TCATAAAAGTGGATGAACATTTTGGCTCTCTGCAAAATGAGTTTCAATCATTTTC 7529
QY 342 GAAACCGAAACCGAAACCTCAACATTCATCACCAGCAATTTTCAGAAAAGAGACGAGTCCA 401
Db 7528 CACATAATCAGGTACAACTGACTCATCACCACAGGAATGACTAAAGGGAGACCCGAC 7469
QY 402 GTGAGTGAGGGTTTGGGAGAAACGACAAAGAAA 435
Db 7468 TTGACGAATGATCTCTGCGAATCTACAAGATACA 7435

RESULT 11
US-09-313-294A-3165

; Sequence 3165, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 3165
; LENGTH: 265
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700611002H1
US-09-313-294A-3165

Query Match 5.6%; Score 35.2; DB 4; Length 265;
Best Local Similarity 68.1%; Pred. No. 0.4;
Matches 49; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 544 AGAAGCAATTCATAGAAAAGTACAACTTCGATATTGTCAATGACGACCGCTTGAAGGTC 603
Db 16 AGCAGGATTCATTGACAAAGTACAACTTCGATTCCTGCAAAACGACTGCCCTCTCCAGGCA 75
QY 604 GCTACAAGTGGG 615
Db 76 GGTTCGAGTGGG 87

RESULT 12
US-09-270-767-7933
; Sequence 7933, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7933
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-7933

Query Match 5.6%; Score 35; DB 4; Length 467;
Best Local Similarity 50.3%; Pred. No. 0.64;
Matches 86; Conservative 0; Mismatches 85; Indels 0; Gaps 0;
QY 400 CAGTGAGTGAGGTTTGGGAGAAACGACAAAGAAATGGAATCATCGCAACGAAGA 459
Db 187 CAAACAGTGTGCGTGTGTAACAAACAACTTAAACCTACAGCAAGAAAACGAAA 246
QY 460 GAAACACACCGGGGTGAGGAAGACTCCAAACGCGCGCGGAGATTGAGGATTTGTTCTCGG 519
Db 247 AAAAAAACGAAACGAAACGAAACGAAAGGATAGTGCCTAAAAAGTGTATAATTCGTATACCA 306
QY 520 AGCTAGAGAGTCCAGACCATAGAGAGAGCAATTCATAGAAAAGTACAACT 570
Db 307 AAGTCGAGAGATCTCTGTAAATTTAGTCAAAAAAAGAAAAAAT 357

RESULT 13
US-09-270-767-23215
; Sequence 23215, Application US/09270767
; Patent No. 6703491

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; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23215
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; US-09-270-767-23215

Query Match          5.6%; Score 35; DB 4; Length 467;
Best Local Similarity 50.3%; Pred. No. 0.64;
Matches 86; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy 400 CAGTGTGAGGTTTGGAGAAACGACAAAGAAATGGAATCATCATCGGCAACGAGA 459
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 187 CAAACAGTGTGTGCGTGTGTAACCAAAACTTAAAAACCTACAGCAAGAAAAACGAAA 246

Qy 460 GAAACACACGGGGTGTAGGAGACTCCAACGGCGCGAGATTGAGGATTGTCTCGG 519
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 247 AAAAAAAACGAAACGAAACGAAAGGATGTGCGCTAAAGTGATTAATTCGTATACCA 306

Qy 520 AGCTAGAGATCCAGACGATAGAAAGCAATTCATAGAAAAAGTACAACT 570
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 307 AAGTCGAGAGATCTCTGTAATTAGTCAAAAAAGAAAAAGAAAAAT 357

RESULT 14
US-09-583-110-608/c
; Sequence 608, Application US/09583110
; Patent No. 669703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: Path00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 608
; LENGTH: 954
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
; US-09-583-110-608

Query Match          5.6%; Score 35; DB 4; Length 954;
Best Local Similarity 52.4%; Pred. No. 0.98;
Matches 77; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 320 AGATCTGGAGGATCATCAATCGAAACCGAAACCTCAACATTCATCACCAGCAA 379
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 783 AGATCTCGGATTGCCCAAAATGAGGTCGGAACCAACAAAAAAGGTTCATCAGCAGAGA 724

Qy 380 TTTCAGAAAAGACGAGTCCAGTCAGTCAGTGAGTGGAGAAAACGACACAGAAATGGA 439
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 723 AAGAAAAACAAGATAGGAGACCGACTACAAAGGCTATAGTCAAGGGAAATCTGAAAAATTT 664

Qy 440 ATCATCATCGGCAACGAGAGAAAAACA 466
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 663 AACATCCCTTCAATGGAGTAAAAAAA 637

RESULT 15
```

```

US-09-107-433-686/c
; Sequence 686, Application US/09107433
; Patent No. 680744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 686:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1104 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...1104
; SEQUENCE DESCRIPTION: SEQ ID NO: 686:
US-09-107-433-686

Query Match          5.6%; Score 35; DB 4; Length 1104;
Best Local Similarity 52.4%; Pred. No. 1.1;
Matches 77; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 320 AGATCTGAGGATCATCAAAATCGAAACCGAAACCGAAACCTCAACATTCATCACCAGCAA 379
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 933 AGATGTCGGATTGCCCAAAATGAGGTCGGAACCAACAAAAAAGGTTCATCAGCAGAGA 874

Qy 380 TTTCAGAAAAGACGAGTCCAGTCAGTCAGTCAGTGGAGAAAACGACACAGAAATGGA 439
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 873 AAGAAAAACAAGATAGGAGACCGACTACAAAGGCTATAGTCAAGGGAAATCTGAAAAATTT 814

Qy 440 ATCATCATCGGCAACGAGAGAAAAACA 466
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 813 AACATCCCTTCAATGGAGTAAAAAAA 787

Search completed: September 30, 2005, 10:08:15
Job time : 164 secs
```

Result No.	Score	Query Match	Length	DB	ID	Description
1	612.8	97.9	824	9	US-09-733-507-7	Sequence 7, Appli
2	612.8	97.9	824	18	US-10-451-139-7	Sequence 7, Appli
3	122	19.5	642	9	US-09-733-507-8	Sequence 8, Appli
4	122	19.5	642	18	US-10-451-139-8	Sequence 8, Appli
5	50.2	8.0	1040	18	US-10-424-599-69339	Sequence 69339, A
6	48.8	7.8	1261	18	US-10-424-599-69348	Sequence 69348, A
7	47.2	7.5	1237	18	US-10-424-599-40086	Sequence 40086, A

THE UNIVERSITY OF CHICAGO

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Db 84 TTCAAGCACAAGCTTCTCACCACCTGAAGAAACGAAGCTTAAATGATTTCTTCTGATTCATC 143
QY ACCGACTCTCATGAGCTCATCGTCTTCGGGTTTTCATCTTCTTCGTTGCTTCGTCGGC 190
Db 144 ACCGACTCTCATGAGCTCATCGTCTTCGGGTTTTCATCTTCTTCGTTGCTTCGTCGGC 203
QY GCTTTAGCGTCTGATGAATGTTCCGTTTACCATCGGTGGAGAAAGTGAATCAGTCCCTC 250
Db 204 GCTTTAGCGTCTGATGAATGTTCCGTTTACCATCGGTGGAGAAAGTGAATCAGTCCCTC 263
QY GAGTATCAGCTCCGGTTGTTTCCACAGTGAATCGAAAGAAATCGCGAAGAAACAGTTCGTC 310
Db 264 GAGTATCAGCTCCGGTTGTTTCCACAGTGAATCGAAAGAAATCGCGAAGAAACAGTTCGTC 323
QY GTTTCGTTAGATCTGAGGATCATCAATCGAAACCGAAACCGAAACCGAAACCTCAACATTCAT 370
Db 384 GTTTCGTTAGATCTGAGGATCATCAATCGAAACCGAAACCGAAACCGAAACCTCAACATTCAT 383
QY CACAGCAATTTTCAGAAAGAGACGAGTCCAGTGAATCGAAAGAAACCGAAACCGAAACCTCAAC 430
Db 384 CACAGCAATTTTCAGAAAGAGACGAGTCCAGTGAATCGAAAGAAACCGAAACCGAAACCTCAAC 443
QY AGAAATGGAATCATCATCGCAACGAAGAGAAACCAACCGGGGGTGAAGAAAGTCCCAAC 490
Db 444 AGAAATGGAATCATCATCGCAACGAAGAGAAACCAACCGGGGGTGAAGAAAGTCCCAAC 503
QY GCGCGCGAGATTGAGGATTTGTTCTCGGAGCTAGAGAGTCCAGACGATAGAGAAAGCA 550
Db 504 GCGCGCGAGATTGAGGATTTGTTCTCGGAGCTAGAGAGTCAAGACGATAGAGAAAGCA 563
QY ATTATAGAAAGTACAACCTTCGATTTGTCAATGACGAAACCGCTTTGAAGGTTCGCTCAA 610
Db 564 ATTATAGAAAGTACAACCTTCGATTTGTCAATGACGAAACCGCTTTGAAGGTTCGCTCAA 623
QY 611 GTGGATCGACTTTAA 626
Db 624 GTGGATCGACTTTAA 639

RESULT 2

US-10-451-139-7
; Sequence 7, Application US/10451139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: WANG, HONG
; APPLICANT: ZHOU, YONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; APPLICANT: AGRICULTURE AND AGRIFOOD CANADA
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 824
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-451-139-7

Query Match 97.9%; Score 612.8; DB 18; Length 824;
Best Local Similarity 99.7%; Pred. No. 3.7e-181;
Matches 614; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 11 ACCCAAAATCCAGAGAGAAAAAATGAGCGAGAGAAAGCGAGAGCTTGAGAGAGAGC 70
|||

Db 24 ACACAAAAATCCAAAGAGAGAAAAAATGAGCGAGAGAAAGCGAGAGCTTGAGAGAGAGC 83
QY 71 TTCAAGCACAAGCTTCTCACCACCTGAAGAAACGAAGCTTAAATGATTTCTTCTGATTCATC 130
Db 84 TTCAAGCACAAGCTTCTCACCACCTGAAGAAACGAAGCTTAAATGATTTCTTCTGATTCATC 143
QY 131 ACCGACTCTCATGAGCTCATCGTCTTCGGGTTTTCATCTTCTTCGTTGCTTCGTCGGC 190
Db 144 ACCGACTCTCATGAGCTCATCGTCTTCGGGTTTTCATCTTCTTCGTTGCTTCGTCGGC 203
QY 191 GCTTTAGCGTCTGATGAATGTTCCGTTTACCATCGGTGGAGAAAGTGAATCAGTCCCTC 250
Db 204 GCTTTAGCGTCTGATGAATGTTCCGTTTACCATCGGTGGAGAAAGTGAATCAGTCCCTC 263
QY 251 GAGTATCAGCTCCGGTTGTTTCCACAGTGAATCGAAAGAAATCGCGAAGAAACAGTTCGTC 310
Db 264 GAGTATCAGCTCCGGTTGTTTCCACAGTGAATCGAAAGAAATCGCGAAGAAACAGTTCGTC 323
QY 311 GTTTCGTTAGATCTGAGGATCATCAATCGAAACCGAAACCGAAACCTCAACATTCAT 370
Db 324 GTTTCGTTAGATCTGAGGATCATCAATCGAAACCGAAACCGAAACCTCAACATTCAT 383
QY 371 CACAGCAATTTTCAGAAAGAGACGAGTCCAGTGAATCGAAAGAAACCGAAACCTCAAC 430
Db 384 CACAGCAATTTTCAGAAAGAGACGAGTCCAGTGAATCGAAAGAAACCGAAACCTCAAC 443
QY 431 AGAAATGGAATCATCATCGCAACGAAGAGAAACCAACCGGGGGTGAAGAAAGTCCCAAC 490
Db 444 AGAAATGGAATCATCATCGCAACGAAGAGAAACCAACCGGGGGTGAAGAAAGTCCCAAC 503
QY 491 GCGCGCGAGATTGAGGATTTGTTCTCGGAGCTAGAGAGTCCAGACGATAGAGAAAGCA 550
Db 504 GCGCGCGAGATTGAGGATTTGTTCTCGGAGCTAGAGAGTCAAGACGATAGAGAAAGCA 563
QY 551 ATTATAGAAAGTACAACCTTCGATTTGTCAATGACGAAACCGCTTTGAAGGTTCGCTCAA 610
Db 564 ATTATAGAAAGTACAACCTTCGATTTGTCAATGACGAAACCGCTTTGAAGGTTCGCTCAA 623
QY 611 GTGGATCGACTTTAA 626
Db 624 GTGGATCGACTTTAA 639

RESULT 3

US-09-733-507-8
; Sequence 8, Application US/09733507
; Patent No. US20010025379A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan
; TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth
; TITLE OF INVENTION: Regulators
; FILE REFERENCE: 81601-3
; CURRENT APPLICATION NUMBER: US/09/733,507
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: CA 2,256,121
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-733-507-8

Query Match 19.5%; Score 122; DB 9; Length 642;
Best Local Similarity 63.0%; Pred. No. 2.7e-27;
Matches 305; Conservative 0; Mismatches 140; Indels 39; Gaps 6;
QY 164 TTCAATCTTCTTCGTTGCTTCGTCGGGCTTTAGCGTCTCATGAATGTTCCGTTACCAT 223
Db 153 TTCTCTTCTTCTTCGCTTACTCGTTTCAGATTCGGAGGTTTCTGCTCCGTCGGCTT 212
QY 224 CGGTGAGAGAAAGTGAATCA--GTCTCTCGAGTATCAGCTCCGGTTGTTTCAACAGTGA 280

Db	213	ATCTGAAGAAGAAGACGATCATCTTAAGCTCAAGCATCAGCTCTGGTTGTTCCAGCAGCGA	272
Qy	281	ATCCAAAGAAATCGGAAGAACAGTTCGTCGTTTGGTGAGATCTGGAGGATCATCAAAAT	340
Db	273	AACTTACGAATTCGCTACTCGTCTTCCATTTTC-----AGATCTGGAGGCTCATGAAT	326
Qy	341	CGAAACCGAAACCGAAACCTCAACATTCATCACCAAGCAATTTTCAGAAAAAGACAGATCC	400
Db	327	CT---CCGAAACCGAAATCTCAACGTTACTACCAACAATTTTCAGAAAAACGGGAATTTC	383
Qy	401	AGTCAGTGAAGGTTTGGAGAAAAAGCAACACGAATAATGGAATCATCATCGGCACCGAAGAG	460
Db	384	ATCAAGCGAGAAATCTGGGAGAA---ACAGCAGAAATGCACTCGGCAGCACCGAGTGTGAG	440
Qy	461	AAACACACCGGGGTGAGAGA-----CTCCAAACGGCGCGGAGAT	502
Db	441	AGATTCAGAGAAAGACGGAGAAAGAGAGATGGAAAAATCATCCGACCGACGCGAGAGCT	500
Qy	503	TGAGGATTTGTTCTTCGGAGCTAGAGAGTCCAGACGATAAAGAAGACAAATTCATAGAAAA	562
Db	501	TGATGACTTTTCTTCGGCGCGGAGAG-----ATACGAAACGAAACGATTCACAGAAAA	554
Qy	563	GTACAACCTCGATATTTGTCATAGCAACCGCTTGAAGTTCGCTACAAGTGGGATTCGACT	622
Db	555	GTACAACCTACGACATCGTCAATGATACGCCGCTTGAAGGTCGGTACCAGTGGTGTAGTCT	614
Qy	623	TTAA	626
Db	615	GAAG	618

RESULT 4
 US-10-451-139-8
 ; Sequence 8, Application US/10451139
 ; Publication No. US20040098763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WANG, HONG
 ; APPLICANT: ZHOU YONGMING
 ; APPLICANT: FOWKE, LARRY C.
 ; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
 ; APPLICANT: AGRICULTURE AND AGRIFOOD CANADA
 ; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
 ; TITLE OF INVENTION: ACTIVITY
 ; FILE REFERENCE: 4810-62237
 ; CURRENT APPLICATION NUMBER: US/10/451,139
 ; CURRENT FILING DATE: 2003-06-18
 ; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
 ; PRIOR FILING DATE: 2001-12-18
 ; PRIOR APPLICATION NUMBER: US 60/255,908
 ; PRIOR FILING DATE: 2000-12-18
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 8
 ; LENGTH: 642
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-10-451-139-8

	Query Match	19.5%	Score 122;	DB 18;	Length 642;
	Best Local Similarity	63.0%;	Pred. No. 2.7e-27;		
	Matches 305;	Conservative 0;	Mismatches 140;	Indels 39;	Gaps 6;
Qy	164	TTCAATCTTCTTCGGTTCGTCGGCGGCTTTAGCGTCTGATGAATGTTCCGGTTACCAT	223		
Db	153	TTCCCTCTTCTCTGGCTTACTCGGTTTCAGATTCCGGAGGTTTCTGCTCCGTCGCGGTT	212		
Qy	224	CGGTGGAGAGAAAGTGATCA---GTCCTCGAGTATCAGCTCCGGTTGTTTCACCACTGA	280		
Db	213	ATCTGAAGAGAGAACCATCATCTAAGCTCAAGCATCAGCTCTGGTTGTTCCAGCAGCGA	272		
Qy	281	ATCGAAAGAAATCCGGAAGAACAGTTCGTCGTTTGGTGTATGATCTGGAGGATCATCAAAAT	340		

Db	273	AAC	TACGAAATCGCTACTCGTCTTCATTTTC-----AGATCTGGAGGCTCATGAAAT	326
Qy	341	CGA	ACCGAAACCGAAACCTCAACATTTATCACCAGCAATTTTCAGAAAAAGAGACGAGTCC	400
Db	327	CT---	CCGAAACCGAAATCTCAACGTTACTTCACCAACAATTTTCAGGAAACAGGGAATTTTC	383
Qy	401	AGT	GAGTGAAGGTTTGGGAGAAACGACACAGAAATCGGAATCATATCGGCAACGAGAG	460
Db	384	ATC	ACGCGAGAAATCTCGGAGAA---ACACGAGAAATGGGACTCGGCGACGACGGAGATGAG	440
Qy	461	AAA	ACAACACCGGGGTCGAGGAAGA-----CTCCAAACGGCGCGCGAGAT	502
Db	441	AGAT	CAGAGAAAGACCGGAGAGAGAAAGATGGAAAATCACCCGCGCAGGCGCAGGCT	500
Qy	503	TGAG	GATTTTCTTCGGAGCTAGAGAGTCCGACGATAAGAGAAGCAATTCATGAAAA	562
Db	501	TGAT	GACTTTTTCTCGCGCGCGAGAG-----ATACGAACAGAAACGATTCACAGAAA	554
Qy	563	GTC	CAACTTCGATATTGTTCATGACGAAACGGCTTGAAGGTCGCTACAGTGGGATCGACT	622
Db	555	GTC	CAACTACGACATCGTCAATGATACGGCGCTTGAAGGTCGGTACCGTGGGTTAGTCT	614
Qy	623	TTAA	626	
Db	615	GAAA	618	

RESULT 5
US-10-424-599-69339
; Sequence 69339, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K

RESULT 5
 US-10-424-599-69339
 ; Sequence 69339, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 39-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 69339
 ; LENGTH: 1040
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_33625C.1
 US-10-424-599-69339

	Query Match	8.0%	Score 50.2;	DB 18;	Length 1040;
	Best Local Similarity	65.2%;	Pred. No. 0.00012;		
	Matches 92;	Conservative 0;	Mismatches 43;	Indels 6;	Gaps 1;
Qy	479	GAAGACTCCACGGCGCGGAGATTGAGGATTTGTTCTCGAGCTAGAGAGTCACAGCA	538		
Db	447	GAAGACGCCACCAACAGCAGAGATCGAAGAGTTTTTCGGATGCGGA-----AAAGTA	500		
Qy	539	TAAGAAAGAACGAATTTCATAGAAAAAGTACAACTTCGATATTTGTCATAGCAACCGCTTGA	598		
Db	501	CGACGGAACCGGTTACACAGAAGTACAACTTTGATATTGTTAGAGATTTCGCCGTTTGA	560		
Qy	599	AGTTCGCTACAAGTGGGATCG	619		
Db	561	GGGTGCGCTACCAAGTGGGTTG	581		

RESULT 6
US-10-424-599-67348
; Sequence 67348, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 67348
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_3182C.1
US-10-424-599-67348

Query Match 7.8%; Score 48.8; DB 18; Length 1261;
Best Local Similarity 70.7%; Pred. No. 0.00035;
Matches 65; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 525 GAGAGTCAGAGGATAAGAGCAATTTCAGAAAAGTACAACTTCGATATTCGCAAT 584
Db GAAATGAGAGGCTCAGCAAAAAAATTCATTGAGAAAGTACAACTTTGATCCTGTGAAT 787

QY 585 GACGAACCGCTTGAAGGTCGCTACAAAGTGGGA 616
Db GAGAAAGCCGCTCTCAGGGCGCTATGAATGGGA 819

RESULT 7
US-10-424-599-40086
; Sequence 40086, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 40086
; LENGTH: 1237
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_136198C.1
US-10-424-599-40086

Query Match 7.5%; Score 47.2; DB 18; Length 1237;
Best Local Similarity 72.6%; Pred. No. 0.0011;
Matches 61; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 535 ACGATAAGAAGCAATTCATAGAAAAGTACAACTTCGATATTCGCAATTCGCAACGCGC 594
Db AAGCAATTCAGAAAGCAATTCAGACAGATCAATATGATATTTGTAAGGACGTACCGC 855

QY 595 TTGAAGGTCGCTACAAAGTGGGATC 618
Db TGAAGGACGCTACGAGTGGGTTTC 879

RESULT 8
US-10-424-599-92958
; Sequence 92958, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 92958
; LENGTH: 1360
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_54956C.1
US-10-424-599-92958

Query Match 7.5%; Score 47.2; DB 18; Length 1360;
Best Local Similarity 63.0%; Pred. No. 0.0012;
Matches 92; Conservative 0; Mismatches 48; Indels 6; Gaps 1;

QY 477 AGGAAGACTCCAAACGGCGGAGATTGAGGATTTGTTCTCGAGCTAGAGATCCAGAC 536
Db AGAAACATTCCAACGGCTTATGAGATGGAGAGTCTTTGCTTATGCCGAGA-----AG 628

QY 537 GATAAGAGAAGCAATTCATAGAAAAGTACAACTTCGATATTTGCAATTCAGCAACCGCTT 596
Db CAGCAACAAACAATATTTATGCAAGTACAAATTCGACATTTGTCATGAAGTACCTCTG 688

QY 597 GAAGTCTGCTACAAAGTGGGATCGACT 622
Db CCTGGACGGTACGAGTGGGTCGCCAGT 714

RESULT 9
US-09-733-507-15
; Sequence 15, Application US/09733507
; Patent No. US20010025379A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan
; TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth
; TITLE OF INVENTION: Regulators
; FILE REFERENCE: 81601-3
; CURRENT APPLICATION NUMBER: US/09/733,507
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: CA 2,256,121
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 15
; LENGTH: 804
; TYPE: DNA
; ORGANISM: Chenopodium rubrum
US-09-733-507-15

Query Match 7.4%; Score 46.2; DB 9; Length 804;
Best Local Similarity 59.2%; Pred. No. 0.0018;
Matches 100; Conservative 0; Mismatches 63; Indels 6; Gaps 1;

QY 454 CGAAGAGAAACACACCGGGGTGAGGAAGACTCCAAACGGCGGCGAGATTGAGGATTTGT 513
Db CGGCGACGAAATCAACGGTACAGATCAAGATGCCGCTCGATTTCAGAAATCGAAGATTTCT 535

QY 514 TCTCGAGCTAGAGATCCAGACCATTAAGAGAAGCAATTCATAGAAAAGTACAACTTCG 573
Db TTGCTGTGCTGA-----AAAAGATCTCCAGAACGCTTCAGCGAAAAGTACAACTTCG 589

QY 574 ATATTGTCAATGACGAACCGCTTGAAGGTCGCTACAAGTGGGATCGACT 622
Db ACATAGTTAAGGACGTGCCACTGAAAGGTCGTTATGATTGGGTTCCAAT 638

RESULT 10
US-10-451-139-14

```
; Sequence 14, Application US/10451139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: WANG, HONG
; APPLICANT: ZHOU, YONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 804
; TYPE: DNA
; ORGANISM: Chenopodium rubrum
US-10-451-139-14

Query Match          7.4%; Score 46.2; DB 18; Length 804;
Best Local Similarity 59.2%; Pred. No. 0.0018;
Matches 100; Conservative 0; Mismatches 63; Indels 6; Gaps 1;

QY 454 CGAAGAGAAACAAACCGGGGTGAGGAAGACTCCAAACGGCGGAGATTGAGGATTTGCT 513
DB 476 CGCGAGAGAAATCAACGGTACAGATCAAGATCGCGTCTGATTCAGAAATCGAAGATTC 535
QY 514 TCTCGGAGCTAGAGAGTCCAGACGATAGAGAAGCAATTCATAGAAAAGTACAACTTCG 573
DB 536 TTGCTGTTGCTGA-----AAAAGATCTCCAGAAACGCTTCAGCGAAAAGTACAAATTCG 589
QY 574 ATATTGTCATGACGAAACCGCTTGAAGTTCGCTACAAAGTGGATCGAAT 622
DB 590 ACATAGTTAAGGAGCGTCCACTGAAAGGTCGTTATGATTTGGGTTCCAAT 638

RESULT 11
US-09-733-507-5
; Sequence 5, Application US/09733507
; Patent No. US20010025379A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan
; TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth
; TITLE OF INVENTION: Regulators
; FILE REFERENCE: 81601-3
; CURRENT APPLICATION NUMBER: US/09/733,507
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: CA 2,256,121
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 377
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-733-507-5

Query Match          7.3%; Score 45.8; DB 9; Length 377;
Best Local Similarity 62.9%; Pred. No. 0.0016;
Matches 90; Conservative 0; Mismatches 47; Indels 6; Gaps 1;

QY 473 GGTGAGGAAGACTCCAAACGGCGGAGATTGAGGATTTGTTCTCGAGCTAGAGAGTCC 532
DB 181 GATGACGGAGATGCCACCGAATCGGAATTCGAAGATTTTGTGGAAGCTGAGAAACA 240
QY 533 AGACGATAGAGAAGCAATTCATAGAAAAGTACAACTTCGATATTTGTCGAATGACGAACC 592
DB 241 ACTC-----AAAGAAAATTCAGAAGAAGTACAATTTTCGATTTTCGAGAAGGAGAACCC 294
QY 593 GCTTGAAGTTCGCTCAAGTGGG 615
DB 295 ATTAGAAGGACGTTACGAATGGG 317

RESULT 13
US-09-733-507-4
; Sequence 4, Application US/09733507
; Patent No. US20010025379A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan
; TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth
; TITLE OF INVENTION: Regulators
; FILE REFERENCE: 81601-3
; CURRENT APPLICATION NUMBER: US/09/733,507
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: CA 2,256,121
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-733-507-4

; Sequence 14, Application US/10451139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: WANG, HONG
; APPLICANT: ZHOU, YONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 377
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-451-139-4

Query Match          7.3%; Score 45.8; DB 18; Length 377;
Best Local Similarity 62.9%; Pred. No. 0.0016;
Matches 90; Conservative 0; Mismatches 47; Indels 6; Gaps 1;

QY 473 GGTGAGGAAGACTCCAAACGGCGGAGATTGAGGATTTGTTCTCGAGCTAGAGAGTCC 532
DB 181 GATGACGGAGATGCCACCGAATCGGAATTCGAAGATTTTGTGGAAGCTGAGAAACA 240
QY 533 AGACGATAGAGAAGCAATTCATAGAAAAGTACAACTTCGATATTTGTCGAATGACGAACC 592
DB 241 ACTC-----AAAGAAAATTCAGAAGAAGTACAATTTTCGATTTTCGAGAAGGAGAACCC 294
QY 593 GCTTGAAGTTCGCTCAAGTGGG 615
DB 295 ATTAGAAGGACGTTACGAATGGG 317

RESULT 13
US-09-733-507-4
; Sequence 4, Application US/09733507
; Patent No. US20010025379A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan
; TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth
; TITLE OF INVENTION: Regulators
; FILE REFERENCE: 81601-3
; CURRENT APPLICATION NUMBER: US/09/733,507
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: CA 2,256,121
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-733-507-4
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Best Local Similarity 62.9%; Pred. No. 0.0018;
Matches 90; Conservative 0; Mismatches 47; Indels 6; Gaps 1;

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Db 199 GATGACGGAGATGCCAACGGAAATCGAAATTTGTTGGAAGCTGAGAAACA 258

QY 533 AGACGATAAGAAAGCAATTCATAGAAAAGTACAACTTCGATATTGTCAATGACGAACC 592
Db 259 ACTC-----AAAGAAAATTCAGAGAAGTACAAATTCGATTTCGAGAAGGAGAAGCC 312

QY 593 GCTTGAAGTCGCTACAAGTGGG 615
Db 313 ATTAGAAGGACGTTACGAATGGG 335

RESULT 14
US-10-451-139-5
; Sequence 5, Application US/10451139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: WANG, HONG
; APPLICANT: ZHOU, YONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; APPLICANT: AGRICULTURE AND AGRIFOOD CANADA
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Sequence: alternative cDNA iCK1c
US-10-451-139-5

Query Match 7.3%; Score 45.8; DB 18; Length 443;
Best Local Similarity 62.9%; Pred. No. 0.0018;
Matches 90; Conservative 0; Mismatches 47; Indels 6; Gaps 1;

QY 473 GGTGAGGAAGACTCCAAACGGCGGAGATTGAGGATTTGTTCTCGGAGCTAGAGAGTCC 532
Db 199 GATGACGGAGATGCCAACGGAAATCGAAATTTGTTGGAAGCTGAGAAACA 258

QY 533 AGACGATAAGAAAGCAATTCATAGAAAAGTACAACTTCGATATTGTCAATGACGAACC 592
Db 259 ACTC-----AAAGAAAATTCAGAGAAGTACAAATTCGATTTCGAGAAGGAGAAGCC 312

QY 593 GCTTGAAGTCGCTACAAGTGGG 615
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RESULT 15
US-09-733-507-3
; Sequence 3, Application US/09733507
; Patent No. US20010025379A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan
; TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth
; TITLE OF INVENTION: Regulators
; FILE REFERENCE: 81601-3

; CURRENT APPLICATION NUMBER: US/09/733,507
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: CA 2,256,121
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-733-507-3

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Best Local Similarity 62.9%; Pred. No. 0.0022;
Matches 90; Conservative 0; Mismatches 47; Indels 6; Gaps 1;

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QY 533 AGACGATAAGAAAGCAATTCATAGAAAAGTACAACTTCGATATTGTCAATGACGAACC 592
Db 432 ACTC-----AAAGAAAATTCAGAGAAGTACAAATTCGATTTCGAGAAGGAGAAGCC 485

QY 593 GCTTGAAGTCGCTACAAGTGGG 615
Db 486 ATTAGAAGGACGTTACGAATGGG 508

Search completed: September 30, 2005, 10:44:35
Job time : 2174 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 30, 2005, 09:05:52 ; Search time 2871 Seconds
(without alignments)
8299.628 Million cell updates/sec

Title: US-09-980-758A-7
Perfect score: 626
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

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2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: * gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gsei: *
9: gb_gsei2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	611.4	97.7	797	3	CNS0A7OL
2	605	96.6	893	3	CNS0A6HI
3	585.6	93.5	664	1	AU237797
4	549.4	87.8	736	3	CNS0A5EV
5	527.8	84.3	784	3	CNS0A6QO
6	299.8	47.9	457	5	BX840619
7	214.2	34.2	425	1	AU228889
8	103.2	16.5	408	5	BP670981
9	96.4	15.4	654	8	BZ426940
10	96.4	15.4	831	8	BH708120
11	95.6	15.3	700	8	BZ083701
12	70.4	11.2	747	7	CO408371
13	70.4	11.2	747	7	CO408372
14	70	11.2	712	7	CV234322
15	70	11.2	919	7	CV242992
16	69.2	11.1	197	8	BZ770063
17	64.2	10.3	1017	5	BO481784
18	60	9.6	774	7	CF212022
19	60	9.6	794	6	CB288800
20	60	9.6	888	7	CF212120
21	58.4	9.3	902	5	BO794660
22	55	8.8	682	7	CO980060
23	53	8.5	672	7	CO986935
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25	52.6	8.4	689	4	BM436399
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27	52.2	8.3	646	6	CD829320
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c 29	51.2	8.2	780	7	CV227354
c 30	51.2	8.2	910	7	CV280549
c 31	50.6	8.1	589	1	AV767700
c 32	50.6	8.1	722	7	CO070046
c 33	50.6	8.1	777	7	CO079308
c 34	50.6	8.1	815	7	CO079309
c 35	49.6	7.9	945	7	CV280994
c 36	49.4	7.9	595	7	CV296057
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c 38	48.8	7.8	573	6	CD396199
c 39	48.8	7.8	733	7	CO981606
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43	48.4	7.7	838	7	CO478922
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45	47.8	7.6	625	5	BU011062

ALIGNMENTS

RESULT 1
CNS0A7OL 797 bp mRNA linear HTC 06-FEB-2004
LOCUS Arabidopsis thaliana Full-length cDNA Complete sequence from clone
DEFINITION GSLTSL9ZE05 of Silique of strain col-0 of Arabidopsis thaliana
(thale cress).
ACCESSION BX826283
VERSION BX826283.1 GI:42466833
KEYWORDS HTC; GSLT cDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 797)
AUTHORS Castelli, V., Aury, J.M., Jallou, O., Wincker, P., Clepet, C.,
Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M.
TITLE Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 797)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jallou O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences) . 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
length
http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
Location/Qualifiers
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FEATURES
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QY 554 CATAGAAAAGTACAACTTCGATATTGTCAATGACCAACCGCTTGAAGGTCGCTACAAGTG 613
 Db 541 CATAGAAAAGTACAACTTCGATATTGTAAATGCAACCGCTTGAAGGTCGCTACAAGTG 600

QY 614 GGATCGACTTTAA 626
 Db 601 GGATCGACTTTAA 613

RESULT 3
 AU237797 664 bp mRNA linear EST 01-APR-2002
 LOCUS RAFL16 Arabidopsis thaliana cDNA clone RAFL16-57-G19 5',
 DEFINITION mRNA sequence.

ACCESSION AU237797.1 GI:19876966
 VERSION AU237797
 KEYWORDS EST.

SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 664)
 Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
 Akiyama, K., Enju, A., Oono, Y., Sakurai, T., Carninci, P., Kawai, J.,
 Itoh, M., Tahii, Y., Arakawa, T., Shibata, K., Shinagawa, A.,
 Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.
 Large scale analysis of Arabidopsis full-length cDNA
 Unpublished (2002)
 Contact: Motoaki Seki

TITLE Plant Functional Genomics Research Group
 JOURNAL RIKEN Genomic Sciences Center
 COMMENT 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-4359
 Fax: 81-298-36-9060
 Email: mseki@rtc.riken.go.jp

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 Best Local Similarity 97.9%; Pred. No. 2.6e-160;
 Matches 602; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 11 ACCCAAAATCCAGAGAGAAAAAATGACGAGAGAAAAAGCGAGCTTCGAGAGAAGC 70
 Db 16 ACACAAATCCAGAGAGAAAAAATGACGAGAGAAAAAGCGAGCTTCGAGAGAAGC 75

QY 71 TTCAGCAACAGTTCTCCACTGAAGAAACGAAGCTTAATGATTTCTGATTCATC 130
 Db 76 TTCAGCAACAGTTCTCCACTGAAGAAACGAAGCTTAATGATTTCTGATTCATC 135

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QY 311 GTTGGTGTAGATCTGGAGGATCATCAATCGAAACCGAAACCGAAACCTCAACATTCAT 370
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QY 371 CACGAGCAATTCAGAAAAGAGACAGTCCAGTGTAGGCGTTGGGAGAAACGACAAC 430
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QY 431 AGAAATGAATCATCATCGCAACGAAGAAAAACAACCGGGGTGAGGAGAACTCCAAAC 490
 Db 436 AGAAATGAATCATCATCGCAACGAAGAAAAACAACCGGGGTGAGGAGAACTCCAAAC 495

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 Db 496 GCGCGCGAGATTGAGGATTTGTTCTCGGAGCTAGAGATCCAGACGATAGAAGAAGCA 555

QY 551 ATTCTAGAAAAGTACAATTCGATATTGTCAATGACGAAACCGCTTGAAGTTCGTACAA 610
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QY 611 GTGGGATCGACTTTA 625
 Db 615 GTGGGATCGACTTTA 629

RESULT 4
 CNS0A6EV 736 bp mRNA linear HTC 06-FEB-2004
 LOCUS Arabidopsis thaliana Full-length cDNA Complete sequence from clone
 DEFINITION GSIL872B03 of Silique of strain col-0 of Arabidopsis thaliana
 (thale cress).

ACCESSION BX826140
 VERSION BX826140.1 GI:42465305
 KEYWORDS HTC; GSILT_cDNA
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 736)
 Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
 Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
 Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.

TITLE Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
 A Combined Approach to Evaluate and Improve Arabidopsis Genome
 Annotation

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 736)
 Genoscope.

TITLE Direct Submission
 JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE [E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr]

COMMENT The sequences are based on single pass reads.
 Life Technologies (a division of Invitrogen)
 full-length libraries construction : Temple G.
 Genoscope members carried out sequencing and annotation : Castelli
 V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
 Schachter V., Weissenbach J., Salanoubat M.
 URV INRA : Clepet C., Caboche M.
 Annotation is based on the June 2003 version of the Arabidopsis
 genome released by MIPS (Munich Information center for Protein
 Sequences). 5 prime and 3 prime are assembled with Phrap.
 http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_RF/Full

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length
http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.

FEATURES
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complement(1..736)
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gene
ORIGIN
Query Match      87.8%; Score 549.4; DB 3; Length 736;
Best Local Similarity 99.8%; Pred. No. 1.1e-143;
Matches 550; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 CAAAATCCAGAGAGAAAAAATCAGCGAGAGAAAGCGAGCTTCGAGAGAGCTTC 60

Qy 74 AAGCAGAGCTTCTCACCACCTGAAGAAACGAAAGCTTAATGATTTCTTGATTCATCACC 133
Db 61 AAGCAGAGCTTCTCACCACCTGAAGAAACGAAAGCTTAATGATTTCTTGATTCATCACC 120

Qy 134 GGACTCTCATGACGTCATCGCTTCGCGGTTTCATCTTCTTCCTCGTTCGTCGGCGGC 193
Db 121 GGACTCTCATGACGTCATCGCTTCGCGGTTTCATCTTCTTCCTCGTTCGTCGGCGGC 180

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Db 481 GCGGAGATTGAGGATTTGTTCTCGAGCTAGAGAGTCAAGACGATAGAGAGAGCAATT 540

Qy 554 CATAGAAAGT 564
Db 541 CATAGAAAGT 551

RESULT 5
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LOCUS
DEFINITION
GSLTSL1872B03 of Silique of strain col-0 of Arabidopsis thaliana
(thale cress).
ACCESSION
BX825610
VERSION
BX825610.1 GI:42464726
KEYWORDS
HTC; GSLT cDNA.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 784)
Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation
Unpublished
2 (bases 1 to 784)
Genoscope.
Direct Submission
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefegenoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life technologies (a division of invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences) . 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
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gene
ORIGIN
Query Match      84.3%; Score 527.8; DB 3; Length 784;
Best Local Similarity 97.1%; Pred. No. 2.4e-143;
Matches 601; Conservative 0; Mismatches 12; Indels 6; Gaps 6;

Qy 14 CAAAATCCAGAGAGAAAAAATGAGCGAGAGAAAGCGAGCTTCGAGAGAGCTTC 73
Db 1 CAAAATCCAGAGAGAAAAAATGAGCGAGATTAAGCGAGAGCTTCGAGAGAGCTTC 60

Qy 74 AAGCAGAGCTTCTCACCACCTGAAGAAACGAAAGCTTAATGATTTCTTGATTCATCACC 133
Db 61 AAGCAGAGCTTCTCACCACCTGAAGAAACGAAAGCTTAATGATTTCTTGATTCATCACC 120

Qy 134 GGACTCTCATGAGCTGCTGCTTCGCGG- TTTCATCTTCTTCGCTTCGCTCGCGCG 192
Db 121 GGACTCTCATGAGCTGCTGCTTCGCGGTTTTCATCTTCTTCGCTTCGCTCGCGCG 180

Qy 193 CTTTAGCGCTCGATGAATGTTCCGTTACCATCGGTGGAGAGAAAGTGATCAGTCTCTCGA 252
Db 181 CTTTAGCATCTGATGAATGTTCCGTTACCATCGGTGGAGAGAAAGTGATCAGTCTCTCGA 240

Qy 253 GTATCAGCTC-CGGTTGTTTTCACC- AGTGAATCGAAAGAAATCGCGAAGAACAGTTCGCTC 310
Db 241 GTATCAGCTCCGGTTGTTTTCACCAGTAAATCGAAGAAATCGGAAGATCAGTTCGCTC 300

Qy 311 GTTTGGTGTAGATCTGGAGAGATCATCAATCGAAACCGAAACCGAAA-CCTCAACATTCA 369
Db 301 GTTTGGTGTAGATCTGGAGAGATCATCAATCGAAACCGAAACCGAAAAGCTTCAACATTCA 360

Qy 370 TCACACGCAATTTTCAGAAAGAGACGAGTCCAGTGAGTGAGGGTTTGGGAGAAACGACAA 429
Db 361 TCACACGCAATTTTCAGAAAGAGACGAGTCCAGTGAGTGAGGGTTTGGGAGAAACGACAA 420
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QY 430 CAGAAATGGAT-CATCATCGG-CAACGAGAGAAAACCAACCGGGGTGAGGAGACTCC 487
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Db 421 CAGAAATGGATGCATCATCGGCAACGAGAGAAAACCAACCGGGGTGAGGAGACTCC 480
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QY 488 AACGGGGCGGAGATTGAGGATTTGTTCTCGAGCTAGAGAGTCCAGACGATAGAAGAA 547
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Db 481 AACGGGGCGGAGATTGAGGATTTGTTCTCGAGCTAAGAGTCAAGACGATAGAAGAA 540
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QY 548 GCAATTCATAGAAAAGTACAATTCGATATTGTCAATGACGAACCCGTTGAAGGTCGCTA 607
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QY 608 CAAAGTCGGATCGACTTTAA 626
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Db 601 CAAAGTCGGATCGACTTTAA 619
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RESULT 6
BX840619
LOCUS
DEFINITION
BX840619 Arabidopsis thaliana Silique Col-0 Arabidopsis thaliana
cDNA clone GSLTSL172ZH03 5PRIM, mRNA sequence.
BX840619
BX840619.1 GI:42534702
EST
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 457)
Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation
Unpublished (2004)
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences).
http://www.genoscope.cns.fr/externe/sequences/Banque_Protet_RF/EST
http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.

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Best Local Similarity 92.1%; Pred. No. 1.5e-76;
Matches 373; Conservative 0; Mismatches 22; Indels 10; Gaps 5;

QY 29 GAAAAAATGAGCGAGAGAAAGCGAGGCTTGAGAGAGCTTCAAGCACAGGCTTCTC 88
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Db 1 GAAAAAATGAGCGAGAGAAAGCGAGAG-TTGAGAGAGAGCTTCAAGCACAGGCTTCTC 59
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QY 89 ACCACTGAAGAAAAAGAACCTTAATGATCTTCTGATTCATCACCGGACTCTCATGACGT 148
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QY 149 CATCGTCTTCGGCGTTTCATCTTCTTCGCTTCGTCGGCGCTTTAGCGTCTGATGA 208
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Db 120 CATCGTCTTCGGCGTTTCATCTTCTTCGCTTCGTCGGCGCTTTAGCGTCTGATGA 179
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QY 209 ATGTTCCGTTACCATCGGTGGAGAGAAAGTATGATCAGTCTCTCGAGTATCAGTCCCGTTG 268
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Db 180 ATGTTCCGTTACCATCGGTGGAGAGAAAGTATGATCAGTCTCTCGAGTATCAGTCCCGTTG 239
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|
|
QY 269 TTTTCCACCGTGAATCGAAGAAAGTATGATCAGTCTCTCGTTCGTT-TGGTGTAGATCTGG 327
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Db 240 TTTTCCACCGTGAATCGAAGAAAGTATGATCAGTCTCTCGTTCGTTATGTTGTAGATCTGG 299
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QY 328 AGGATCATCAAAATCGAAACCGAA--ACCTCAACATTC--TCACCAGCAATTT 382
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Db 300 AGGATCATCAAAATCGAAACCGAAAGAAAGAAAGTACAACTTACACACACAGCGAATTT 359
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QY 383 CAGAAAAAGAGAC---GAGTCCAGTGTAGTGGGTTTGGGAGAAAC 424
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Db 360 CAGAAAAAGAGACAGAGTTCCAAAGTGTAGTCCGCGATAGGATGAAC 404
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RESULT 7
AU228889/c
LOCUS
DEFINITION
AU228889 RAFL16 Arabidopsis thaliana cDNA clone RAFL16-57-G19 3',
mRNA sequence.
AU228889
AU228889.1 GI:19743536
EST
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 425)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
Akiyama, K., Enju, A., Oono, Y., Sakurai, T., Carninci, P., Kawai, J.,
Itoh, M., Teshi, Y., Arakawa, T., Shibata, K., Shinagawa, A.,
Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
details.

FEATURES
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/organism="Arabidopsis thaliana"
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/db_xref="taxon:3702"
/clone="RAFL16-57-G19"
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/clone_lib="RAFL16"
/site="Site_1: BamHI; Site_2: SalI; dark-grown"

ORIGIN
Query Match 34.2%; Score 214.2; DB 1; Length 425;
Best Local Similarity 97.9%; Pred. No. 1.9e-51;
Matches 238; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

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QY	294	CGCAGAACAGATTTCGTGTTGGTTGTAGATCTGGAGGATCATCAATCGAAA	345
DB	252	CCGAGGAAGAGTCCGACTGTTCTCTGTAGATCTGGAGGTGAGATTTTTCGAAA	303
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LOCUS			
DEFINITION	BH708120 831 bp DNA linear GSS 20-FEB-2002		
ACCESSION	genomic survey sequence.		
VERSION	BH708120		
KEYWORDS	BH708120.1 GI:18793934		
SOURCE	GSS.		
ORGANISM	Brassica oleracea		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.		
AUTHORS	Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.		
TITLE	Whole genome shotgun sequencing of Brassica oleracea		
JOURNAL	Unpublished (2001)		
COMMENT	Other GSSs: BOHYL71TR Contact: Chris Town		
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	Location/Qualifiers		
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	/clone_lib="BO 2.3 KB"		
	/note="vector: pHOSt; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOSt using BstXI linkers"		
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Best Local Similarity	64.7%; Pred. No. 7.7e-17;		
Matches 189; Conservative	0; Mismatches 76; Indels 27; Gaps 2;		
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DB	197	GCGCAGCGCTTGAAGCTCCGAGCGCAAGCGACTCGCAACTCAAGAAGAAGAAGCTCGAT	256
QY	114	GATTCCTTCATTCATCACCGGACTCTCATGACGTGATCGTCTTCGCGGTTTCATCTTCT	173
DB	257	GAT-----GACTCTCATGGGCGTCTTCTTCCTCGCGGTTTCCTTCTCCT	298
QY	174	TCCGTTCTGCTTCGTCCGGCGCTTTTAGCGTCTGATGAATGTTCCGTTACCATCGGTGAGAA	233
DB	299	TCCGTGCTTTCATCGGATGATTCCTCTCGAGGCGGATGCTCTGTTACTCGCGCGGAA	358
QY	234	GAAGTGATCAGTCTCTCGAGTATCAGCTCCGGTTGTTTTCACCAAGTGAATCGAAGAAATC	293
DB	359	GACGATGACAAGAGCTCGATCATC-----TGTTTCAGCAGTGAATCGAAGAAATC	409
QY	294	CGCAGAACAGTTTCGTGTTGGTTGTAGATCTGGAGGATCATCAATCGAAA	345
DB	410	CCGAGGAAGAGTCCGACTGTTCTCTGTAGATCTGGAGGTGAGATTTTTCGAAA	461
RESULT 11			
BZ083701			
LOCUS			
DEFINITION	BZ083701 700 bp DNA linear GSS 10-OCT-2002		
ACCESSION	lkk95a11.q1 B.oleracea002 Brassica oleracea genomic survey		

Db	RESULT 15
	CV242992/c
	LOCUS
	DEFINITION
	ACCESSION
	VERSION
	KEYWORDS
	SOURCE
	ORGANISM

[illegible]

Query Match	11.2%;	Score 70;	DB 7;	Length 712;
Best Local Similarity	57.7%;	Pred. No. 4.1e-09;		
Matches 209;	Conservative 0;	Mismatches 135;	Indels 18;	Gaps 4;
Qy	261	TCGGTGTGTTTCCAGTGAATCGAAAGAAATCGCGAAGAACAGTTCGTGCTTGGTGTGA	320	
Db	570	TCTGTGCTCCAGCAATGAATCGATCAAGGTTGTGAAGGACAGCTTGAGGTT---TATA	514	
Qy	321	GATCTGGAGATCATCAAAATCGAAAACCGAAACCGAAACCTCAACATTCATCACACGCAAT	380	
Db	513	GATCTGGAG------CGAAGAGTTCGGAACCGAAAGCTCGACGTGCAATGACAGAAA	460	
Qy	381	TTCCAGAAAAGAGACGAGTCCAGTGTAGTGAAGGTTTGGGAG---AAACGACAAACAGAAATG	437	
Db	459	TTCCAGTAGAGAAACCACTCCTTCAAGCGAGTTTCACGGGATGTACTCGCCGGCAGCCGCTG	490	
Qy	438	GAATCATCATCGGCCAACGAGAGAGAAACAACCGGGGTGAGGAAGACTCCCAACCGCGGGCG	497	
Db	399	GAGAAGAAAGAGAAATCTTCAACGAGAGAAAGTCAACCGCTGTGAAAATGCCGATCAGGCT	340	
Qy	498	GAGATTGAGGATTGTGTTCTCGAGCTAGAGAGTCCAGACGATAAGAAGAACAGCAATTCATA	557	
Db	339	GAGATCGATCGCTTTTTCGCGGGGGCGAGAGA-----GAGAGACGAAAAGATTGTCG	286	
Qy	558	GAAGAAGTACAACCTTCGATATTGTCAATGACGAACCGCTTCAAGGTCGCTACAAGTGGGAT	617	
Db	285	GAGAAGTACAACCTACGATGTTGTGAAGATTTTCCCACTGAGGGGTCCGTACCACTGGATT	226	
Qy	618	CG 619		

Location/Qualifiers

1. .919

organism="Populus balsamifera subsp. trichocarpa"

mol_type="mRNA"

cultivar="Wild clone"

sub_species="trichocarpa"

db_xref="taxon:3694"

clone="WS02516_J17"

sex="Male"

lab_host="E. coli DH10B TI phase resistant cells"

clone_lib="PT-MB-N-A-15"

note="Vector: pBluescript II SK (+) XR; Site_1: EcoRI end of cDNA; Site_2: XhoI (3' end of cDNA); Terminal vegetative buds from 20 year old trees harvested near Corvallis, Oregon on September 19th, 2001. cDNA was prepared from 5 micrograms of mRNA and directionally ligated into the pBluescript II SK (+) XR vector using the pBluescript II XR cDNA Library Construction Kit according to manufacturer's instructions with modifications (Stratagene). Plasmid DNA was then transformed by electroporation into DH10B cells (Invitrogen) for propagation. Normalization was applied according to published methods [Donaldo M.F. et al. (1996) Genome Research 6(9):791] in order to reduce the abundance of highly expressed transcripts."

Query Match	11.2%	Score 70;	DB 7;	Length 919;
Best Local Similarity	57.7%;	Pred. NO. 4.3e-09;		
Matches 209;	Conservative	0;	Mismatches 135;	Indels 18; Gaps 4
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Db	666	TCCTGCTGCTCCAGCAATGAATCGATCAAGTGTGTGAAGGACAGCTTTGAGGTT---TATA	610	
Qy	321	GATCTGGAGGATCATCAAAATGAAACCCGAAACCGAAACCTCAACATTCATCACCAAGCAAT	380	

609	Db	 GATCTGGAG-----CGAAGAGTTCGAAACGGAAGCTCGACGTGCAATGACAGGAAA	556
381	Qy	TTTCAGAAAAGAGACGAGTCCAGTGAGTCAGGCTTTGGGAG--AAACGACAACAGAAATG	437
555	Db	TTTCAGTAGAGACCACTCTTTCAGCGAGTTTCACGGGATGTACTCGCGGACGCCGTG	496
438	Qy	GAATCATCATCGGCAACGAAGAGAAAACAACCGGGGGTGAGGAAGACTCCAACGCGCGCG	497
495	Db	GAGAAGAAAGAAATTCATCAGGAGAAAGTCACCGGCTGTGAAATGCCGAGTCAGGCT	436
498	Qy	GAGATTGAGGATTTGTCTCGAGCTAGAGAGTCCAGACGATAGAAGAAGCAATTCAAT	557
435	Db	GAGATCGATGCGTTTTCGCGGGGGCAGAGAG-----GAGGAGCAGAAAAGATTTGCA	382
558	Qy	GAAAAGTACAACTTCGATATTGTCAATGACGAAACCGCTTGAAAGTCGCTACAAGTGGGAT	617
381	Db	GAGAAGTACAACTACGATGTTGTGAAGGATTTGCCAGTGGAGGGTCGTACCACTGGGATT	322
618	Qy	CG 619	
321	Db	TG 320	

Search completed: September 30, 2005, 11:32:37
Job time : 2876 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 30, 2005, 11:35:38 ; Search time 4142 Seconds
(without alignments)
2444.988 Million cell updates/sec

Title: US-09-980-758A-8
Perfect score: 1045
Sequence: 1 FRDLPNFKKMSRKREL.....NFDVNDPLEGRYKWDRLX 209

Scoring table:

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Ygapext 0.5			
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Fgapext 7.0			
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Delext 7.0			

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

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3: gb.in.*

4: gb.om.*

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6: gb.pat.*

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9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1037	99.2	626	6	BD267733 Method of
2	1007	96.4	824	6	AX008797 Sequence
3	1007	96.4	824	6	AX463066 Sequence
4	1007	96.4	840	8	AF106705 Arabidops

ALIGNMENTS

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LOCUS	BD267733	Method of promoting plant cell proliferation by functionally inhibiting plant cyclin inhibitor gene.	626 bp DNA linear PAT 17-JUL-2003
DEFINITION	BD267733	Method of promoting plant cell proliferation by functionally inhibiting plant cyclin inhibitor gene.	
ACCESSION	BD267733	BD267733.1	GI:33077501
VERSION	BD267733	JP 2002543823-A/4.	
KEYWORDS	BD267733	Arabidopsis thaliana (thale cress)	
SOURCE	BD267733	Arabidopsis thaliana	
ORGANISM	BD267733	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	
REFERENCE	BD267733	1 (bases 1 to 626)	
AUTHORS	BD267733	Roberts, J. and Kelly, B.	
TITLE	BD267733	Method of promoting plant cell proliferation by functionally inhibiting plant cyclin inhibitor gene	
JOURNAL	BD267733	Patent: JP 2002543823-A 4 24-DEC-2002;	
COMMENT	BD267733	FRED HUTCHINSON CANCER RESEARCH CENTER	
	OS	Arabidopsis thaliana (thale cress)	
	PN	JP 2002543823-A/4	
	PD	24-DEC-2002	
	PF	15-MAY-2000 JP 2000618299	
	PI	14-MAY-1999 US 60/134373	
	PC	A01H5/00,C12N5/10,C12N15/09,C12N15/00,C12N5/00 CC	Method of
		Promoting plant cell proliferation by functionally	CC
		inhibiting	

AJ301557 Arabidops
AP000419 Arabidops
AX008798 Sequence
AX463067 Sequence
AJ301558 Arabidops
AF208692 Arabidops
AC011807 Arabidops
AB029483 Pisum sat
AY085749 Arabidops
AX008791 Sequence
AX463060 Sequence
AY439104 Glycine m
AJ517189 Nicotiana
U94772 Arabidopsis
CQ803686 Sequence
BD267732 Method of
AJ251851 Arabidops
AX463077 Sequence
AY088290 Arabidops
A98054 Sequence 1
AR490032 Sequence
BD075687 Cyclin-de
AK176528 Arabidops
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AX008793 Sequence
AX463062 Sequence
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AY439101 Glycine m
AK176575 Arabidops
AK175492 Arabidops
AX008805 Sequence
AX463073 Sequence
AJ002173 Chenopodi
AK117586 Arabidops
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AX463065 Sequence

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Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      99.23%      Indels:      0
DB:              6      Gaps:      0
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DB      3 CGAGATTACCCAAATAATCCAGAGAGAAAAAATGACGAGAGAGAAACGAGAGCTTCCA 62
QY      22 GluGluAlaSerSerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSer 41
DB      63 GNAGAGGCTTCNAGCACAGCTTCTCACCACTGAGAGAAACGAAGCTTAATGATTTCTCT 122
QY      42 AspSerSerProAspSerHisAspValIleValPheAlaValSerSerSerValAla 61
DB      123 GATTTCATCACCGACTCTCATGACGTCATCGTCTCCGCGTTTCATCTTCTCCGTTGCT 182
QY      62 SerSerAlaAlaLeuAlaSerAspGluCysSerValThrIleGlyGluGluSerAsp 81
DB      183 TCGTCGGCGGCTTTAGCTGCTGATGAATGTTCCGTTTACCATCGGTGGAGAGAAAGTGAT 242
QY      82 GlnSerSerSerIleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsn 101
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QY      102 SerSerSerPheGlyValAspLeuGluAspHisGlnIleGluThrGluThrSer 121
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QY      122 ThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGluGlyLeuGlyGlu 141
DB      363 ACATTTCATCACCGCAATTTCAGAAAGAGACGAGTCCAGTGAGTGGGGTTTGGGAGAA 422
QY      142 ThrThrThrGluMetGluSerSerSerAlaThrLysArgLysGlnProGlyValArgLys 161
DB      423 ACGACAAACAGAAATCGAATCATATCGGACGAGAGAGAAACAACCGGGGGTGGGAGAG 482
QY      162 ThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLys 181
DB      483 ACTCAACCGCGCGGAGATTGAGGATTGTTCTCGGAGCTAGAGAGTCCAGACGATTAAG 542
QY      182 LysLysGlnPheIleGluLysTyrAsnPheAspIleValAsnAspGluProLeuGluGly 201
DB      543 AAGAAGCAATTATAGAAAGTACAACTTCGATATTTGTAATGACGAACCGCTTGAAGGT 602
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DEFINITION Sequence 7 from Patent WO9964599.
ACCESSION AX008797
VERSION AX008797.1 GI:9996261
KEYWORDS
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SOURCE
ORGANISM Arabidopsis thaliana (thale cress)
          Arabidopsis thaliana
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          rosids; eurosids II; Brassicales; Brassicaceae; Arabidopeis.
REFERENCE
AUTHORS 1
TITLE   Fowke,L.C., Wang,H. and Crosby,W.L.
JOURNAL Cyclin-dependent kinase inhibitors as plant growth regulators
        Patent: WO 9964599-A 7 16-DEC-1999;
        FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD
        (CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV
        SASKATCHEWAN TECHNOLOGIES (CA)
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AUTHORS De Veylder, L., Beeckman, T., Beemster, G.T., Krols, L., Terras, F.,
Landrieu, I., van der Schueren, E., Maes, S., Naudts, M. and Inze, D.
TITLE Functional analysis of cyclin-dependent kinase inhibitors of
Arabidopsis
JOURNAL Plant Cell 13 (7), 1653-1668 (2001)
MEDLINE 21342510
PUBMED 11449057
REFERENCE 2 (bases 1 to 591)
AUTHORS de Veylder, L.
TITLE Direct Submission
JOURNAL Submitted (31-OCT-2000) De Veylder L., Departement Plantegenetica,
Vlaams Interuniversitair Instituut voor Biologie (VIB), K.L.
Ledeganckstraat 35, B-9000 Gent, BELGIUM
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REFERENCE

AUTHORS Kaneko,T., Katoh,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S.
 TITLE Structural analysis of Arabidopsis thaliana chromosome 3. II.
 JOURNAL Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC
 MEDLINE DNA Res. 7 (3), 217-221 (2000)
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 Kaneko,T., Katoh,T., Sato,S., Nakamura,Y., Asamizu,E. and Tabata,S.
 TITLE Direct Submission
 JOURNAL Submitted (03-SEP-1999) Yasukazu Nakamura, Kazusa DNA Research
 Institute, Department of Plant Gene Research, 1532-3, Yana,
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 Tel:81-438-52-3935, Fax:81-438-52-3934)
 COMMENT Address for correspondence: kaos@kazusa.or.jp
 For the latest information on annotation of this clone, please see
 http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=Mv111
 Genes with similarity to proteins in the databases are described in
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 protein similarity are described as 'unknown protein'.
 The software programs used to predict genes include: Grail
 (Informatics Group, Oak Ridge National Laboratory,
 http://compbio.ornl.gov/Grail-1.3/),
 GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
 NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
 Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
 SplicePredictor (Volker Brendel, Stanford University,
 http://gremli.zool.iastate.edu/cgi-bin/sp.cgi).
 Genes encoding tRNAs are predicted by tRNAscan-SE
 (Sean Eddy, Washington University School of Medicine, St. Louis,
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 This sequence may not be the entire insert of this clone. It may be
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KRNFGKHNKTWDSLQSSLSIGRVSVALLGCTVFFSLKLSGRISQLOSMPIYSVA
RPHSESDFLWKTSGNFRKNLDSVNRNGIVGNIKVLIDMLKMHCGSHPDALYLSKSG
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VESIFCLCMQNTAQTAEAKSCYRFVLLHLEVLQAHIPEDGIAEAGAEIEALLEEA
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/note="unnamed protein product; gene_id:MV111.9
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Alignment Scores:

Pred. No.:	3.92e-58	Length:	81875
Score:	837.00	Matches:	200
Percent Similarity:	57.14%	Conservative:	0
Best Local Similarity:	57.14%	Mismatches:	3
Query Match:	80.10%	Indels:	149
DB:	8	Gaps:	3

US-09-980-758A-8 (1-209) x AF000419 (1-81875)

Qy	6	LysAsnProArgGluLysMetSerGluArgLysArgGluLeuAlaGluGluAlaSer	25
Db	12777	AAAAATCAAGAGAGAAAAAATGAGCGAGAGAACGAGAGCTTGCAGAGAGAGCTTCA	12718
Qy	26	SerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerAspSerPro	45
Db	12717	AGCAACAGCTTCTCACCACCTGAAGAAAAACGAGCTTAATGATTTCTCTGATTCATCACCG	12658
Qy	46	AspSerHisAspValIleValPheAlaValSerSerSerSerValAlaSerSerAlaAla	65
Db	12657	GACTCTCATGACGTATCGTCTTCGCGGTTTCATCTCTTCGTTGCTTCGTCGCGGCT	12598
Qy	66	LeuAlaSerAspGluCyseSerValThrIleGlyGlyGluGluSerAspGlnSerSerSer	85
Db	12597	TTAGGCTGATGATGTTCCGTTACCATCGTGCAGAGAGAAAGTGATCAGTCTCTCGAGT	12538
Qy	86	IleSerSerGlyCysePheThrSerGluSerLysGluIleAlaLysAsnSerSerSerPhe	105

Db	12537	ATCAGCTCCGGTTGTTTTCACCAAGTGAATCGAAAGAAATCGCGAAAGACAGTTCGTGTTT	12478
Qy	106	GlyValAspLeuGlu	110
Db	12477	GGTGTAGATCTGGAGGTGAATTTTCAAAATCAAAATAACTCTCTCTACTTGAATCGATT	12418
Qy	111	-----As	111
Db	12417	AATCAGACGATTTTCTCAGTTTTCGTTTGTGATTTTATTTTCCGTTTCTGTGTTTCAGGA	12358
Qy	111	PhiGlnIleGluThrGluThrGluThrSerThrPheIleThrSerAsnPheArg	129
Db	12357	TCATCAATCGAAACCGAAACCTCAACATTCATCCAGCAATTTTCAG-GTTCA	12299
Qy	129	-----	129
Db	12298	TAATCTTTTGTTCCTCCCTCCCAAAATAGAGTTCAATCGATTATTTATCTCTCTGG	12239
Qy	130	-----LysGluThrSerProValSerGluGlyLeuG	140
Db	12238	CGATTTTCTCTGTTTATGCGAGAAAGACGAGTCCAGTGAAGGTTTGGG	12179
Qy	140	YgluThrThrThrGluMetGluSerSerSerAlaThrLysArgLysGlnProGlyVal	160
Db	12178	AGAAACGACACACAGAAATGGAATCATCATCGCAACGAAAGAGAAACACCGGGGTGAG	12119
Qy	160	qLysThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAs	180
Db	12118	GAAAGCTCCAAACGGCGGGAGATTTGAGATTGTTCTCGAGGCTAGAGAGTCAAGACGA	12059
Qy	180	pLysLysGlnPheIleGluLys	188
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Qy	188	-----	188
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Qy	188	-----	188
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Qy	188	-----	188
Db	11879	TAAAAAGATTAAACCGACGCTAGTTAGCAAAATATCTTAAAGAGAGAGAGATCAGAAATC	11820
Qy	189	-----TyrAsnPheAspIleValIleAsnGluProle	199
Db	11819	CTAACGAAACACACACTTTGGCAGAGTCAACTTCGATATTGTCAATGACGAACCGCT	11760
Qy	199	uGluGlyArgTyrLysTrpAspArgLeu	208
Db	11759	TGAAGGTGCTACAGTGGGATCGACTT	11732
RESULT 7			
LOCUS	AX008798	Sequence 8 from Patent WO9964599.	642 bp
DEFINITION	AX008798		linear
ACCESSION	AX008798		
VERSION	AX008798.1	GI:9996262	
KEYWORDS			
SOURCE			
ORGANISM			
	Arabidopsis thaliana		
	Arabidopsis thaliana		
	Arabidopsis thaliana (thale cress)		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
	rosids; eurosids I; Brassicales; Brassicaceae; Arabidopsi		
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
	Fowke,L.C., Wang,H. and Crosby,W.L.		
	Cyclin-dependent kinase inhibitors as plant growth regulators		
	Patent: WO 9964599-A 8 16-DEC-1999;		
	FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD		
	(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV		
	SASKATCHEWAN TECHNOLOGIES (CA)		

REFERENCE

- Fowke, L.C., Wang, H. and Zhou, Y.
Modulation of plant cyclin-dependent kinase inhibitor activity
Patent: WO 0250292-A 8 27-JUN-2002;
University of Saskatchewan Technologies (CA); Minister of Agriculture and Agrifood Canada (CA)

FEATURES

Location/Qualifiers	
1..642	/organism="Arabidopsis thaliana"
	/mol_type="unassigned DNA"
	/db_xref="taxon:3702"

ORIGIN

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Alignment Scores:
Pred. No.:      1.98e-20          Length:       642
Score:         351.50           Matches:     93
Percent Similarity: 58.85%        Conservative:   30
Best Local Similarity: 44.50%      Mismatches:    57
Query Match:    33.64%            Indels:       29
DB:             Gaps:            10
                                         10

US-09-980-758A-8 (1-209) x AX463067 (1-642)

QY   9  ArgGluLysLYseMetSerGluArgLysergLeuAlaGluGluAlaSerSerThrSer 28
      ||||| :||||: |::|: |::|: |::|: |::|: |::|: |::|: |::|: |::|:
Db   31 AGAGAAATGAGCGAACAAAACCCCAAGAAGAGATTCTTGATCAGGAAGGATCAAAC----- 84

QY   29 PheSerProLeuLYsThrLYsLeuAsnAspSerSerAsp-----SerSerProAsp 36
      ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||:
Db   85 -----ATCACAGAGATGAGACTGCATCATGATGATGATGATGATGATGATGATGATGATGAT 135

QY   47 SerHisAspValIleValPheAlaValSerSerSerValAlaSerSerAlaLaLeu 66
      ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||:
Db   136 AGA-----ACTCTTCTTTCTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCG 177

QY   67 AlaSerAspGlu-----CysSerValThrIleGlyGlyGluGluSerAspGln--- 82
      ||||| :||||: |::|: |::|: |::|: |::|: |::|: |::|: |::|:
Db   178 GTTTCAGATTCGGAGGTTCCTGCTGCCCTCCGTTATCTGAAGAAGAAAGACGATCATCTA 233

QY   83 SerSerSerIleSerSerGLyCyaphethrSerGluSerLYsGluIleAlaLYsAsnSer 102
      ||||| :||||: |::|: |::|: |::|: |::|: |::|: |::|: |::|:
Db   238 ACTCAGCATCAGCTCTGGTGTTCMGACAGCGAAACTAACGAAATACGCTACTCGTCTT 297

QY   103 SerSerPheGlyValAspLeuGluAspHisGlnIleGluThrGluThrGluThrSerThr 122
      ||||| :||||: |::|: |::|: |::|: |::|: |::|: |::|: |::|:
Db   298 CCATTT-----TCAGATCTGGAGCTCATGAATC-- -TCCGAAACCGAAATCTCAACG 348

QY   123 PheIleThrSerAsnPheArgLYSGluThrSerProValSerGluGlyLeuGlyGluThr 142
      ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||:
Db   349 TTACTCACCACAATAATTCAGGAAACAGCGGAATTTTCATCAAGCGAGAAATCTGGGAGAAACA 408

QY   143 -----ThrThrGluMetGluSerSerSerAlaThrLYsAtgLvsBgLn 150
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QY   157 ProGlyValArgLYsThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGlu 176
      ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||:
Db   469 AAG---ATGGAAAAATCACCCGACGAGCTTGATGACTTTTTCTCGGGCGGGAG 529

QY   177 SerProAspAspLYsLYSGlnPheIleGluLYSTyrLenPheAspIleValAsnAsp 196
      ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||: ::||:
Db   526 AGATACGAA-----CAGAAACGATTACAGAAAAGTAGAACACTACGACATCGTCAATGAT 579

QY   197 GluProLeuGluGYatqTYrLYSTrp 205
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Db   580 ACGCCGCTTGAAGGTTCGGTACAGTGG 606

RESULT 9
ATH301558
LOCUS ATH301558 588 bp mRNA linear PLN 26-JUL-2000
DEFINITION Arabidopsis thaliana mRNA for cyclin-dependent kinase inhibitor 7 (krp7 gene).
ACCESSION AJ301558

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Alignment Scores:

Pred. No.:	5.09e-17	Length:	4116	
Score:	323.00	Matches:	67	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	30.91%	Indels:	0	
DB:	8	Gaps:	0	
US-09-980-758A-8 (1-209) X AF208692 (1-4116)				
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QY	26	SerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerSerPro 45		
Db	3975	AGCACAAAGCTTCACCACTCGAAGAAACGAAGCTTAATGATTTCTGATTCATCACCG 4034		
QY	46	AspSerHisAspValIleValPheAlaValSerSerSerValAlaSerSerAlaAla 65		
Db	4035	GACTCTCATGACGTATCGTTCGCGGTTCACTTCCTCGTTCGTCGCGGCT 4094		
QY	66	LeuAlaSerAspGluCysSer 72		
Db	4095	TTAGCGTCTGATGAATGTTCC 4115		
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LOCUS	AC011807	104679 bp	DNA	linear
DEFINITION	Arabidopsis thaliana chromosome I BAC F14J22 genomic sequence,			
ACCESSION	AC011807			
VERSION	AC011807.4	GI:6693374		
KEYWORDS	HTG.			
SOURCE	Arabidopsis thaliana (thale cress)			
ORGANISM	Arabidopsis thaliana			
REFERENCE	Eukaryota: Viridiplantae; Streptophyta: Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 104679)			
AUTHORS	Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vysotskaia,V.S., Walker,M., Yu.G., Ecker,J., Theologis,A. and Davis,R.W. Unpublished			
JOURNAL	2 (bases 1 to 104679)			
REFERENCE	Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Nguyen,M., Lam,B., Southwick,A., Bel,Q., Buehler,E., Chin,C., Chlou,J., Choi,E., Dunn,P., Gonzalez,A., Howng,B., Kim,C., Koo,T., Lee,J.M., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S., Mukharasy,N., Pham,P., Sakano,H., Schwartz,J., Shinn,P., Thaveri,A., Toriumi,M., Vaysberg,M., Walker,M., Yu.G., Ecker,J., Theologis,A. and Davis,R.W. Direct Submission			
JOURNAL	Submitted (15-OCT-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA			
REFERENCE	3 (bases 1 to 104679)			
AUTHORS	Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vysotskaia,V., Walker,M., Yu.G., Ecker,J., Theologis,A. and Davis,R.W. Direct Submission			
JOURNAL	Submitted (14-JAN-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA			
REFERENCE	4 (bases 1 to 104679)			
AUTHORS	Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A. and Davis,R.W. Direct Submission			
JOURNAL	Submitted (13-SEP-2000) DNA Sequencing and Technology Center,			

COMMENT

Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
 On Jan 14, 2000 this sequence version replaced gi:6692246.
 Bases 92948-104679 of IGF clone F14J22 overlap with bases 1-11732 of IGF clone F13F21 (gb|AC007504).
 e-mail for correspondence: arab@sequence.stanford.edu
 Genes with similarity to proteins in the databases are named 'putative', '-like' or 'similar to'. Genes that have EST similarity but no significant protein similarity are described as 'unknown proteins'. Genes that are annotated based only on gene prediction software are described as 'hypothetical proteins'. The gene prediction programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge, http://genes.mit.edu/GENSCAN.), FEXA (Victor Solovyev, http://genomic.sanger.ac.uk/gf/gf.shtm), and NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/NetPlantGene.html).

FEATURES

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 /db_xref="taxon:3702"
 /chromosome="I"
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 DIETSLSELVSESLALLVLLHMTETECEAVASPSRVGPTRLFLDSSIRVNAA
 ALIENVLTAQSMGLKLIISGSDSIFEGVLDLILKNPISRRALKIGIKAFALCLVQK
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Db      71032  GACCCACACACGCGCATGATAGCAGATCCTTAACCTTGCGAGTTGTTTAAAC-ATGT 71090
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Db      71091  ATAGGTACAACTACGACATCGTCAATGATACGCGCTTGAAGTTCGTCACCACTGG 71146

RESULT 12
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DEFINITION complete cds.
ACCESSION AB029483
VERSION   AB029483.1 GI:12081914
KEYWORDS  cyclin dependent kinase inhibitor.
SOURCE    Pisum sativum
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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          rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;
          Pisum.
REFERENCE 1 (bases 1 to 927)
AUTHORS   Shimizu-Sato,S. and Mori,H.
TITLE     A cDNA from Pisum sativum encoding the cyclin-dependent kinase
          inhibitor (CKI) homologue
JOURNAL   Published Only in DataBase (2001)
REFERENCE 2 (bases 1 to 927)
AUTHORS   Shimizu-Sato,S. and Mori,H.
TITLE     Direct Submission
JOURNAL   Submitted (01-JUL-1999) Sae Shimizu-Sato, Nagoya University,
          Graduate School of Bioagricultural Sciences; Chikusa, Nagoya, Aichi
          464-8601, Japan (E-mail:saes@agr.nagoya-u.ac.jp,
          Tel:+81-52-789-4166, Fax:+81-52-789-4296)
FEATURES
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ORIGIN
Alignment Scores:
Pred. No.: 1,56e-06 Length: 927
Score: 187.00 Matches: 59
Percent Similarity: 46.35% Conservative: 30
Best Local Similarity: 30.73% Mismatches: 83
Query Match: 17.89% Indels: 20
DB: 8 Gaps: 6

US-09-980-758A-8 (1-209) x AB029483 (1-927)

Qy      20  LeuAlaGluGluAlaSerSerPheSerProLeuLysLysThrLysLeuAsnAsp 39
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Db      96  TTAGCCATGAGCCACAGTTTCACTCCACGACCTACAAAGAGAAGAAAGATCAACAGA 155

Qy      40  SerSerAspSerSerProAspSerHisAspValIleValPheAlaValSerSerSer 59
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Db      156  ACCGAAACCGTAAA-----TCTCAACCGCTCAACCGAAG 191

Qy      60  ValAlaSer-----SerAlaAlaLeuAlaSerAspGluCysSerValThrIleGlyGly 77
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Db      192  ATAGCGACGGTTAGGCCGGAACCGGTAAACGGAGAAACATTCCTCGGTTCTACCTCCGAT 251

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Qy      78  GluGluSerAspGlnSerSerIleSerSerGlyCysPheThrSerGluSerLysGlu 97
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Db      252  GAAGAATTTCCGCGCATCGTGTGTTTCAAGCAACCGGATCCGTTGAACCTCGATGAAGAAG 311

Qy      98  IleAlaLysAsnSerSerPheGlyValAspLeuGluAspHisGlnIleGluThrGlu 117
       :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      312  ATCAAA-----TCGTTAGATCTCGAGGTGGAGAGCGCGCAAGGTGAA 353

Qy      118  ThrGluThrSerThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGlu 137
       |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      354  ACGTCGACGTGCAATTCGATGAAGAAATTTGAGAGGAGAGATGATGCTTCAAGCGAG 413

Qy      138  GlyLeuGlyGluThrThrGluMetGluSerSerSerAlaThrLysArgLysGln--- 156
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Db      414  TTTTCGAGGA---AATTCTCAGAGCTTGAGTCAATGGAGACCAATTTCTCGCGCTCCGATT 470

Qy      157  ProGlyValArgLysThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGlu 176
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Db      471  TCATCTCCCAAAAGACGCCAAGCAATACGAGCTTGAGGAATTTTTCGCTGCTGCTGAG 530

Qy      177  SerProAspAspLysLysGlnPheIleGluLysTyrAsnPheAspIleValAsnAsp 196
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Db      531  AAA-----GACATTCAAGAAATTTCAAGAAAGTAAATATGATATCTTGAAGGAC 584

Qy      197  GluProLeuGluGlyArgTyrLysTyrAspArgLeu 208
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Db      585  GTTCGCTTGAAGGACGCTACGAGTGGGTTCAAGTTG 620

RESULT 13
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LOCUS     Arabidopsis thaliana clone 17682 mRNA, complete sequence.
DEFINITION
ACCESSION AY085749
VERSION   AY085749.1 GI:21404459
KEYWORDS  FLJ.CDNA.
SOURCE    Arabidopsis thaliana (thale cress)
ORGANISM  Arabidopsis thaliana
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          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
          1 (bases 1 to 780)
REFERENCE 1 (bases 1 to 780)
AUTHORS   Haas,B.J., Volkovsky,N., Town,C.D., Troukhan,M., Alexandrov,N.,
          Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.
TITLE     Full-length messenger RNA sequences greatly improve genome
          annotation
JOURNAL   Genome Biol. 3 (6), RESEARCH0029 (2002)
MEDLINE   22088475
PUBMED    12093376
REFERENCE 2 (bases 1 to 780)
AUTHORS   Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
          Feldmann,K.
TITLE     Full-length cDNA from Arabidopsis thaliana
JOURNAL   Unpublished
REFERENCE 3 (bases 1 to 780)
AUTHORS   Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
          Feldmann,K.
TITLE     Direct Submission
JOURNAL   Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
          Malibu, CA 90265, USA
COMMENT   This clone sequence is one of 5,000 Ceres full-length cDNAs made
          available to TIGR and Genbank. The following quality assessment of
          this set was done by comparison with known proteins: two percent of
          the clones are estimated to be 5'-truncated; less than one percent
          are 3'-truncated; approximately two percent represent alternative
          splice variants, including unspliced introns and spliced exons; one
          percent may contain premature stop codons; five percent may have
          frame shifts in a coding region. A sequence is considered to be
          5'-truncated if it lacks the translation initiation start (ATG). A
          sequence is considered to be 3'-truncated if it lacks the
          C-terminal end of the encoded protein. Please note that these cDNA
          sequences are derived from the Ws or Laer ecotypes and therefore
          may contain polymorphisms when compared to sequences from Col-0.

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241 -----ATACATCTGGAGGAGGAAGATAAAGATGCTGAC

[illegible]

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QY 140 -----GlyGluThrThrGluMetGluSerSerSerAlaThrLysArgLysGln 156
Db 415 TGTGTAGCGGAGGAGAAACCATGAGGAGACGCTGACGCGGAGGAGGAGGAGGAGCG 474
QY 157 ProGlyValArgLysThrProThrAlaAlaGluLeuAspLeuPheSerGluLeuGlu 176
Db 475 AATTTGATGACGAGAGATGCCACCGAATCGGAATTTGAAGATTTTGTGGAGAGCTGAG 534
QY 177 SerProAspLysLysLysGlnPheIleGluLysTyAsnPheAspIleValAsnAsp 196
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LOCUS AX463060 905 bp DNA linear PAT 15-JUL-2002
DEFINITION Sequence 1 from Patent WO0250292.
ACCESSION AX463060
VERSION AX463060.1 GI:21886074
KEYWORDS
SOURCE
ORGANISM Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1
Fowke, L.C., Wang, H. and Zhou, Y.
Modulation of plant cyclin-dependent kinase inhibitor activity
Patent: WO 0250292-A 1 27-JUN-2002;
University of Saskatchewan Technologies (CA); Minister of
Agriculture and Agrifood Canada (CA)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:3702"
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Best Local Similarity: 27.16% Mismatches: 68
Query Match: 17.32% Indels: 66
DB: 6 Gaps: 10

US-09-980-758A-8 (1-209) x AX463060 (1-905)

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Db 44 CCTAAATCGAAGATGGTGAGAAAATATAGAAAAGCTAAA---GGAATTTGTAGAAAGCTGGA 100
QY 25 SerSerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerSer 44
Db 101 GTTTCGTCAACGTATATGACGTACGAGCGCGGAGA----- 136
QY 45 ProAspSerHisAspValIleValPheAlaValSerSerSerSerValAlaSerAla 64
Db 137 -----ATTGTTATGTTAGATCGGAAAAATCA----- 163
QY 65 AlaLeuAlaSerAspGluCysSerValThrIleGlyGluSerAspGlnSerSer 84

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Search completed: September 30, 2005, 13:02:26
Job time : 4189 secs

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Db 164 -----AGCTCTGCTCTCGTCTCGTGTGAT-----AAT 190
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Db 191 GGAGTTTCGTCGCTTGT-----AGTGAAGCAATGAATATATAAGAAAGAAATTA--- 241
QY 105 PheGlyValAspLeuGluAspHisGlnIleGluThrGluThrGluThrSerThrPhe--- 123
Db 242 -----ATACATCTGGAGGAGGAGAAATAAGATGGTGACACTGAAACGTCGACGTATCGA 295
QY 124 -----lleThrSerAsnPheArgLysGlu----- 131
Db 296 CCGGGTACGAGAGGAGAGCTTTTGAATAATCTCAGAGAGAGAGAGAGAAAGAAATTAAGT 355
QY 132 -----ThrSerProValSerGluGlyLeu----- 139
Db 356 AATCCATGAGAGAAATTTATTCATCGGAATTTGAATCGCGGTTAAAGAAATCGTTAGATTGT 415
QY 140 -----GlyGluThrThrThrGluMetGluSerSerSerAlaThrLysArgLysGln 156
Db 416 TGTGTAGCGGAGGAGAAACCATGAGGAGACGCTGACGCGGAGGAGGAGGAGGAGCG 475
QY 157 ProGlyValArgLysThrProThrAlaAlaGluLeuAspLeuPheSerGluLeuGlu 176
Db 476 AATTTGATGACGAGAGATGCCACCGAATCGGAATTTGAAGATTTTGTGGAGAGCTGAG 535
QY 177 SerProAspLysLysLysGlnPheIleGluLysTyAsnPheAspIleValAsnAsp 196
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QY 197 GluProLeuGluGlyArgTyLysTrpAspArgLeu 208
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Run on: September 30, 2005, 11:34:08 ; Search time 531 Seconds
(without alignments)
2329.992 Million cell updates/sec

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Fgapop 6.0 , Fgapext 7.0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1007	96.4	824	3 AAZ29417	Aaz29417 Arabidops
3	1007	96.4	824	6 AAD40765	Aad40765 Arabidops
4	351.5	33.6	642	3 AAZ29418	Aaz29418 Arabidops
5	351.5	33.6	642	6 AAD40766	Aad40766 Arabidops

6	181	17.3	779	3 AAC47352	Aac47352 Arabidops
7	181	17.3	780	3 AAC36958	Aac36958 Arabidops
8	181	17.3	904	3 AAZ29415	Aaz29415 Arabidops
9	181	17.3	905	6 AAD40761	Aad40761 Arabidops
10	177	16.9	630	12 ADN72202	Adn72202 Thale cre
11	177	16.9	809	5 AAC85204	Aac85204 Plant D-1
12	177	16.9	861	6 AAD40770	Aad40770 Arabidops
13	177	16.9	883	3 AAC45711	Aac45711 Arabidops
14	177	16.9	886	3 AAC37798	Aac37798 Arabidops
15	177	16.9	932	2 AAX25015	Aax25015 Arabidops
16	172	16.5	1116	3 AAN02402	Aan02402 Cyclin de
17	172	16.5	1116	3 AAA95288	Aaa95288 Soybean c
18	168.5	16.1	804	3 AAZ29420	Aaz29420 Chenopodi
19	168.5	16.1	804	6 AAD40768	Aad40768 Chenopodi
20	162.5	15.6	870	3 AAA95293	Aaa95293 Arabidops
21	162.5	15.6	870	3 AAC46465	Aac46465 Arabidops
22	162.5	15.6	870	12 ADN72346	Adn72346 Thale cre
23	162.5	15.6	1290	6 AAD40769	Aad40769 Arabidops
24	159	15.2	755	3 AAZ29416	Aaz29416 Arabidops
25	159	15.2	755	6 AAD40764	Aad40764 Arabidops
26	155	14.8	797	6 AAD40771	Aad40771 Arabidops
27	153	14.6	875	2 AAX25016	Aax25016 Arabidops
28	153	14.6	1242	6 ABK93958	Abk93958 DNA encod
29	152	14.5	669	12 ADN72350	Adn72350 Thale cre
30	151	14.4	1067	6 ABK93971	Abk93971 Full leng
31	150.5	14.4	533	3 AAZ29419	Aaz29419 Arabidops
32	150.5	14.4	533	6 AAD40767	Aad40767 Arabidops
33	148.5	14.2	1022	6 ABN98442	Abn98442 Arabidops
34	147.5	14.1	609	3 AAA95279	Aaa95279 Wheat cyc
35	147.5	14.1	1169	3 AAA95292	Aaa95292 Wheat cyc
36	144	13.8	443	6 AAD40763	Aad40763 Arabidops
37	140.5	13.4	1341	3 AAC33295	Aac33295 Arabidops
38	139	13.3	377	6 AAD40762	Aad40762 Arabidops
39	139	13.3	1260	13 ADR85800	Adr85800 Aspergill
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43	139	13.3	1755	13 ADR85928	Adr85928 Aspergill
44	139	13.3	2117	13 ADR85341	Adr85341 Aspergill
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ALIGNMENTS

RESULT 1
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ID AAC85201 standard; DNA; 626 BP.
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AC AAC85201;
XX
DT 22-MAR-2001 (first entry)
XX
DE Plant D-like cyclin inhibitor BRO4 coding sequence.
KW Plant; D-like cyclin inhibitor gene; BRO4; hyperplastic; variant;
KW growth rate; dividing cells; inactivation; protoplast; seed; root cell;
KW meristem; leaf; ss.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT CDS 36..626
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XX
PN WO200069883-A1.
XX
PD 23-NOV-2000.
XX
PR 15-MAY-2000; 2000WO-US013379.
XX
PR 14-MAY-1999; 99US-0134373P.
XX

PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.
XX
PI Roberts J, Kelly B;
XX
XX WPI; 2001-024998/03.
DR P-PSDB; AAB47001.
XX
XX Functionally inactivating expression of plant D-like cyclin inhibitor
PT gene for producing a hyperplastic variant plant, modulating the growth
PT and/or yield of plants, and increasing the proportion of dividing cells.
XX
PS Claim 16; Page 41; 50pp; English.
XX
XX The sequence given in AAC85201 represents a plant D-like cyclin inhibitor
CC gene, BRO4. This sequence may be used to produce a hyperplastic variant
CC plant, increase the growth rate of a plant, or increase the proportion of
CC dividing cells in a plant cell population, relative to a wild-type plant,
CC by functionally inactivating the expression of a plant D-like cyclin
CC inhibitor gene in a plant. This sequence is homologous to a sequence
CC present in a D-like cyclin inhibitor gene and when integrated at the
CC corresponding locus, functionally inactivates plant D-like cyclin
CC inhibitor protein expression. BRO4 is useful for producing hyperplastic
CC variant plants, increasing the growth rate of a plant and for increasing
CC the proportion of dividing cells in a plant cell population comprising
CC protoplast, seeds, root cells, meristem cells or leaf cells
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SQ Sequence 626 BP; 202 A; 131 C; 156 G; 137 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,99e-89 Length: 626
Score: 1037.00 Matches: 207
Percent Similarity: 100.00% Conservative: 0
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Query Match: 99.23% Indels: 0
DB: 5 Gaps: 0

US-09-980-758A-8 (1-209) x AAC85201 (1-626)

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DB 3 CGAGATTTCACCAAAATCCAGAGAGAAAAATGAGCGAGAGAAACGAGAGCTTCA 62

QY 22 GluGluAlaSerSerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSer 41
DB 63 GAAGAAGCTTCAAGCACAGCTTCTCACCACTGAAGAAACGAAGCTTAATGATCTTCT 122

QY 42 AspSerSerProAspSerHisAspValIleValPheAlaValSerSerSerSerValAla 61
DB 123 GATTTCATCCCGGACTCTCATGACGTCATCGTCTTCGCGGTTTCATCTTCTCGTTCGT 182

QY 62 SerSerAlaAlaLeuAlaSerAspGluCysSerValThrIleGlyGluGluSerAsp 81
DB 183 TCGTCGGCGGCTTTAGCGTCTGATGAATGTTCCGTTACCATCGGTGGAGAAAGTGTAT 242

QY 82 GlnSerSerSerIleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsn 101
DB 243 CAGTCTCGATATCAGTCTCGGTGTTTCCACAGTGAATCGAAGAATCGGAGAAC 302

QY 102 SerSerSerPheGlyValAspLeuGluAspHisGlnIleGluThrGluThrSer 121
DB 303 AGTTCGTGTTGGTGTAGATCTGAGGATCATCAATCGAAACCGAAACCGAAACCTCA 362

QY 122 ThrPheIleThrSerAspPheArgLysGluThrSerProValSerGluGlyLeuGlyGlu 141
DB 363 ACATTTCATCCAGCAATTTAGAAAAAGAGACGAGTCCAGTGAGTGGGGTTTGGAGAA 422

QY 142 ThrThrThrGluMetGluSerSerSerAlaThrLysArgLysGlnProGlyValArgLys 161
DB 423 ACGCAACAGAAATGAAATCATCATCGCAGCAGAGAGAAACAACACCGGGGTGAGGAG 482

QY 162 ThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLys 181
DB 483 ACTCCACCGGGCGGAGATTGAGGATTGTTCTCGGAGCTAGAGAGTCCAGACGATTAAG 542

QY 182 LysLysGlnPheIleGluLysTyrAsnPheAspIleValAsnAspGluProLeuGly 201
DB 543 AAGAGCAATTCATAGAAAAGTCAACTTCGATATTGTCATGACGAACCGCTTGAAGT 602

QY 202 ArgTyrLysTyrAspArgLeu 208
DB 603 CGCTACAAGTGGGATCGACTT 623

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XX AC AAZ29417;
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XX DT 29-FEB-2000 (first entry)
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XX DE Arabidopsis thaliana CDK inhibitor, ICN2 encoding cDNA.
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XX KW Cyclin-Dependent kinase inhibitor; CDK; Interactor of Cyclin 2; ICN2;
KW Cdc2a; D-class cyclin; CycD1; CycD2; CycD3; morphogenesis;
KW antisense construct; tissue-specific promoter; transgenic plant;
KW male sterility; ds.
XX
XX OS Unidentified.
XX
XX FH Key Location/Qualifiers
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XX PN WO9964599-A1.
XX
XX PD 16-DEC-1999.
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XX PF 08-JUN-1999; 99WO-CA000532.
XX
XX PR 08-JUN-1998; 98CA-02235978.
XX
XX PR 31-DEC-1998; 98CA-02256121.
XX
XX PA (MTAC) AGRIC & AGRIFOOD CANADA.
XX
XX PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
XX
XX PA (CANA) NAT RES COUNCIL CANADA.
XX
XX PI Wang H, Powke LC, Crosby WL;
XX
XX DR WPI; 2000-097540/08.
XX
XX DR P-PSDB; AAY44337.
XX
XX PT Modifying plant cell development using nucleic acid encoding inhibitor of
PT cyclin-dependent kinase, or corresponding antisense sequence, e.g. for
PT inducing male sterility.
XX
XX PS Disclosure; Fig 4; 58pp; English.
XX
XX CC The present sequence is a cDNA encoding ICN2 which inhibits A. thaliana
CC Cyclin-Dependent kinase (CDK). Interactor of Cyclin 2 (ICN2) interacts
CC with Cdc2a, D-class cyclins, CycD1, CycD2 and CycD3 and shares functional
CC and sequence similarity with ICK1. Growth, morphogenesis, multiplication,
CC and segment differentiation and maturation of plant cells can be
CC modified by transforming them with nucleic acid encoding CDK inhibitor or
CC antisense construct complementary to the inhibitor gene, operably linked
CC to a tissue-specific promoter. The transgenic plants exhibit alteration
CC of traits such as petals, male sterility and ability to set seeds
XX
SQ Sequence 824 BP; 287 A; 164 C; 185 G; 188 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3e-86 Length: 824
Score: 1007.00 Matches: 202
Percent Similarity: 99.51% Conservative: 0
Best Local Similarity: 99.51% Mismatches: 1
Query Match: 96.36% Indels: 0

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DB: 3 Gaps: 0
US-09-980-758A-8 (1-209) x AAZ29417 (1-824)

QY 6 LysAsnProArgGluLysLysMetSerGluArgLysArgGluLeuAlaGluAlaSer 25
DB 28 AAAAAATCCAAGAGAGAGAAAAAATGACGAGAGAGAAACGAGAGCTTCAGAGAGAGTTCA 87
QY 26 SerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerSerPro 45
DB 88 AGCACACAGCTTCTCACCACCTGAAGAAACGAAGCTTAATGATCTCTGATTCATCACCG 147
QY 46 AspSerHisAspValIleValPheAlaValSerSerSerValAlaSerSerAlaAla 65
DB 148 GACTCTCATGACGTATCGTCTTCGCGGTTTCATCTTCCTTCGTCGCGGCT 207
QY 66 LeuAlaSerAspGluCysSerValThrIleGlyGluGluSerAspGlnSerSer 85
DB 208 TTAGCGTCTGATGAATGTTCCGTTTACCATCGGTGGAGAGAAAGTATGATCTCTGCTCGGCT 267
QY 86 IleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSerSerPhe 105
DB 268 ATCAGCTCCGGTGTGTTCCACAGTGAATCGAAAGAAATCGCGAAGAACAGTTCGTCGTTT 327
QY 106 GlyValAspLeuGluAspHisGlnIleGluThrGluThrGluThrSerThrPheIleThr 125
DB 328 GGTGTAGATCTGAGGATCATCAATCGAAACCGAAACCGAAACCTCAACATTCATCACCC 387
QY 126 SerAsnPheArgLysGluThrSerProValSerGluGlyLeuGlyGluThrThrGlu 145
DB 388 AGCAATTTCAAGAAAGAGAGAGTCCAGTGAGTGAGGGTTTGGAGAAACGACACAGAA 447
QY 146 MetGluSerSerSerAlaThrLysArgLysGlnProGlyValArgLysThrProThrAla 165
DB 448 ATGGAATCATATCGCGAACAGAGAGAAACCAACCGGGGTGAGGAAGACTCCACCGCG 507
QY 166 AlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLysLysGlnPhe 185
DB 508 GCGGAGATTGAGGATTTGTTCTCGGAGCTAGAGAGTCAAGACGATAAAGAAAGCAATTC 567
QY 186 IleGluLysTyrAsnPheAspIleValAsnAspGluProLeuGluGlyArgTyrLysTrp 205
DB 568 ATAGAAAAGTACAACTTCGATATTGTCAATGACGAACCGCTTGAAGGTCGCTACAAAGTG 627
QY 206 AspArgLeu 208
DB 628 GATCGACTT 636

RESULT 3
AAD40765
ID AAD40765 standard; cDNA; 824 BP.
XX
AC AAD40765;
XX
DT 30-OCT-2002 (first entry)
XX
DE Arabidopsis thaliana ICN2 cDNA.
XX
KW Plant development; cyclin-dependent kinase; CDK inhibitor; ICN1; ICN2;
KW ICN2; ICN6; ICN7; ICN8; ICN9; ICN10; ICN11; ICN12; ICN13; ICN14;
KW plant breeding; growth; gene; ss.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
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FT 49..639
FT CDS
FT /tag= b
FT /product= "ICN2 protein #2"
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XX WO200250292-A2.
PN 27-JUN-2002.
XX
XX 18-DEC-2001; 2001WO-CA001825.
XX
XX 18-DEC-2000; 2000US-0255908P.
XX
XX (MIAC ) CANADA MIN AGRIC & AGRI-FOOD CANADA.
XX (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
XX
XX Wang H, Zhou Y, Fowke LC;
XX
XX WPI; 2002-519888/55.
XX P-PSDB; AAE25103, AAE25104.
XX
XX Modifying plant development, e.g. growth or maturation, which is
XX particularly useful in plant breeding, by introducing nucleic acids
XX coding for cyclin-dependent kinase (CDK) inhibitor, cyclin or proteins
XX that bind to CDK inhibitors.
XX
XX Disclosure; Fig 4; 89pp; English.
XX
XX The invention relates to a method for the development of a plant. The
XX method involves introducing into a plant cell a nucleic acid encoding a
XX protein that binds or interacts with a cyclin-dependent kinase (CDK)
XX inhibitor polypeptide (such as ICK1, ICK2, ICN2, ICN6, ICN7, ICN8 and
XX ICN9), a cyclin polypeptide, a CDK, or a polypeptide that modulates the
XX degradation of a CDK inhibitor polypeptide. The method is useful for
XX modifying the growth and development of plants e.g. morphogenesis,
XX growth, multiplication, enlargement, differentiation or maturation of a
XX cell or plant. It is particularly useful in plant breeding. The present
XX sequence is A. thaliana ICN2 cDNA
XX
XX Sequence 824 BP; 287 A; 164 C; 185 G; 188 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3e-86 Length: 824
Score: 1007.00 Matches: 202
Percent Similarity: 99.51% Conservative: 0
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Query Match: 96.36% Indels: 0
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US-09-980-758A-8 (1-209) x AAD40765 (1-824)

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DB 28 AAAAAATCCAAGAGAGAGAAAAAATGACGAGAGAGAAACGAGAGCTTCAGAGAGAGTTCA 87
QY 26 SerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerSerPro 45
DB 88 AGCACACAGCTTCTCACCACCTGAAGAAACGAAGCTTAATGATCTCTGATTCATCACCG 147
QY 46 AspSerHisAspValIleValPheAlaValSerSerSerValAlaSerSerAlaAla 65
DB 148 GACTCTCATGACGTATCGTCTTCGCGGTTTCATCTTCCTTCGTCGCGGCT 207
QY 66 LeuAlaSerAspGluCysSerValThrIleGlyGluGluSerAspGlnSerSer 85
DB 208 TTAGCGTCTGATGAATGTTCCGTTTACCATCGGTGGAGAGAAAGTATGATCTCTGCTCGGCT 267
QY 86 IleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSerSerPhe 105
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QY 126 SerAsnPheArgLysGluThrSerProValSerGluGlyLeuGlyGluThrThrGlu 145
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Qy	166	AlaGluIleGluAspLeuPheSerGluLeuGluSerProAspLysLysLysGlnPhe	185
Db	508	GCGGAGATTGAGGATTTGTTCTCGAGCTAGAGAGTCAAGACGATAGAGAAGCAATTC	567
Qy	186	IleGluLysTyrAsnPheAspIleValAsnAspGluProLeuGluGlyArgTyrLysTrp	205
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Qy	206	AspArgLeu 208	
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ID	AAZ29418	standard; cDNA; 642 BP.	
XX	AAZ29418;		
DT	29-FEB-2000	(first entry)	
DE	Arabidopsis thaliana	CDK inhibitor, ICN6 encoding cDNA.	
KW	Cyclin-Dependent kinase inhibitor; CDK; Interactor of Cyclin 6; ICN6;		
KW	Cdc2a; D-class cyclin; CycD1; CycD2; CycD3; morphogenesis;		
KW	antisense construct; tissue-specific promoter; transgenic plant;		
KW	male sterility; ds.		
OS	Unidentified.		
Key	Location/Qualifiers		
CDS	1..624		
FT	/*tag= a		
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XX	WO9964599-A1.		
XX	16-DEC-1999.		
XX	08-JUN-1999;	99WO-CA000532.	
XX	08-JUN-1998;	98CA-02235978.	
XX	31-DEC-1998;	98CA-02256121.	
XX	(MIAC) AGRIC & AGRIFOOD CANADA.		
PA	(UUSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.		
PA	(CAN)) NAT RES COUNCIL CANADA.		
XX	Wang H, Fowke LC, Crosby WL;		
XX	WPI: 2000-097540/08.		
XX	P-PSDB; AAY44338.		
XX	Modifying plant cell development using nucleic acid encoding inhibitor of		
XX	cyclin-dependent kinase, or corresponding antisense sequence, e.g. for		
XX	inducing male sterility.		
XX	Disclosure; Fig 5; 58pp; English.		
XX	The present sequence is a cDNA encoding ICN6 which inhibits A. thaliana		
XX	Cyclin-Dependent kinase (CDK). Interactor of Cyclin 6 (ICN6) interacts		
XX	with Cdc2a, D-class cyclins, CycD1, CycD2 and CycD3 and shares functional		
XX	and sequence similarity with ICK1. Growth, morphogenesis, multiplication,		
XX	enlargement, differentiation and maturation of plant cells can be		
XX	modified by transforming them with nucleic acid encoding CDK inhibitor or		
XX	antisense construct complementary to the inhibitor gene, operably linked		
XX	to a tissue-specific promoter. The transgenic plants exhibit alteration		
XX	of traits such as petals, male sterility and ability to set seeds		

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PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
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			SerSerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerAspSerSer 44		
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			ProAspSerHisAspValIleValPheAlaValSerSerSerValAlaSerSerAla 64		

QY 140 -----GlyGluThrThrGluMetGluSerSerAlaThrLysArgLysGln 156
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 Db 589 AAGCCATTAGAGGAGCGTTACGAATGGTAAAGTTA 624

RESULT 9
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 ID AAD40761 standard; cDNA; 905 BP.
 XX
 AC AAD40761;
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 DT 30-OCT-2002 (first entry)
 XX
 DE Arabidopsis thaliana ICK1 cDNA.
 XX
 KW Plant development; cyclin-dependent kinase; CDK inhibitor; ICK1; ICK2;
 KW ICN2; ICN6; ICN7; ICN8; ICN9; ICN10; maturation; enlargement;
 KW plant breeding; growth; gene; ss.
 XX
 OS Arabidopsis thaliana.
 XX
 FH Key Location/Qualifiers
 FT CDS 56..631
 FT FT /*tag= a
 FT FT /product= "ICK1 protein"
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 PN WO200250292-A2.
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 PD 27-JUN-2002.
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 PF 18-DEC-2001; 2001WO-CA001825.
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 XX
 PA (MIRAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
 PA (UUSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
 XX
 PI Wang H, Zhou Y, Fowke LC;
 XX
 DR WPI; 2002-519888/55.
 DR P-PSDB; AAE25101.
 XX
 PT Modifying plant development, e.g. growth or maturation, which is
 PT particularly useful in plant breeding, by introducing nucleic acids
 PT coding for cyclin-dependent kinase (CDK) inhibitor, cyclin or proteins
 PT that bind to CDK inhibitors.
 XX
 PS Disclosure; Fig 1; 89pp; English.
 XX
 CC The invention relates to a method for the development of a plant. The
 CC method involves introducing into a plant cell a nucleic acid encoding a
 CC protein that binds or interacts with a cyclin-dependent kinase (CDK)
 CC inhibitor polypeptide (such as ICK1, ICK2, ICN2, ICN6, ICN7, ICN8 and
 CC ICN9), a cyclin polypeptide, a CDK, or a polypeptide that modulates the
 CC degradation of a CDK inhibitor polypeptide. The method is useful for
 CC modifying the growth and development of plants e.g. morphogenesis,
 CC growth, multiplication, enlargement, differentiation or maturation of a
 CC cell or plant. It is particularly useful in plant breeding. The present
 CC sequence is A. thaliana ICK1 cDNA
 XX
 SQ Sequence 905 BP; 307 A; 107 C; 230 G; 261 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 9, 24e-08 Length: 905
 Score: 181.00 Matches: 63
 Percent Similarity: 42.24% Conservatives: 35
 Best Local Similarity: 27.16% Mismatches: 68
 Query Match: 17.32% Indels: 66
 DB: 6 Gaps: 10

US-09-980-758A-8 (1-209) x AAD40761 (1-905)

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 QY 25 SerSerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerAspSerSer 44
 Db 101 GTTTCGTCAACGTATATGACGTACGAGCCGGAG-- 136
 QY 45 ProAspSerHisAspValIleValPheAlaValSerSerSerSerValAlaSerSerAla 64
 Db 137 -----ATTGTTTATGTTAGATCGGAAATCA----- 163
 QY 65 AlaLeuAlaSerAspGluCysSerValThrIleGlyGlyGluGluSerAspGlnSerSer 84
 Db 164 -----AGCTCTGCTCCGTCGTCGTGAT-----AAT 190
 QY 85 SerIleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSerSerSer 104
 Db 191 GGAGTTTTCGTCGTCCTTGT-----AGTGAAGCAATGAATATAAGAAAGAAATA-- 241
 QY 105 PheGlyValAspLeuGluAspHisGlnIleGluThrGluThrGluThrSerThrPhe--- 123
 Db 242 -----ATACATCTGGAGGAGGAATGAATGTTGACACTGAACCTCGACGTATCGA 295
 QY 124 -----IleThrSerAsnPheArgLysGlu----- 131
 Db 296 CGGGGTACGAAGAGGAGGAGCTTTTGAATACTGAGAGAGGAGGAGGAGGAGGAGGAGTAAAGT 355
 QY 132 -----ThrSerProValSerGluGlyLeu----- 139
 Db 356 AAATCCATCGAGAGATTTATTCATCGGAATTTGAATCGCGGTTAAAGAAATCGTAGATTGT 415
 QY 140 -----GlyGluThrThrThrGluMetGluSerSerSerAlaThrLysArgLysGln 156
 Db 416 TGTTCAGCGGAGGAGAAACGATGAGGAGACGGTCAGCGGAGGAGGAGGAGGAGGAGCG 475
 QY 157 ProGlyValArgLysThrProThrAlaAlaGluLeuGluAspLeuPheSerGluLeuGlu 176
 Db 476 AAATTGATGACGCGAGATGCCACGGAATCGGAATTTGAAGATTTTGTGGAAGCTGAG 535
 QY 177 SerProAspAspLysLysGlnPheIleGluLysTyrAsnPheAspIleValAsnAsp 196
 Db 536 AAA-----CAACTCAAGAAATAATCAAGAAAGTACAATTCGATTCGAGAAGGAG 589
 QY 197 GluProLeuGluGlyArgTyrLysTrpAspArgLeu 208
 Db 590 AAGCCATTAGAGGAGCGTTACGAATGGTAAAGTTA 625

RESULT 10
 ADN72202
 ID ADN72202 standard; cDNA; 630 BP.
 XX
 AC ADN72202;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Thale cress cDNA upregulated in E2Fa/Dpa expressing plants SeqID 97.
 KW gene; ss; plant; transgenic; E2Fa/Dpa transcription factor;
 KW growth regulator; animal feed product; thale cress;
 KW cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
 XX

OS Arabidopsis thaliana.
 PN WO2004035798-A2.
 XX 29-APR-2004.
 XX 20-OCT-2003; 2003WO-EP011658.
 XX 18-OCT-2002; 2002EP-00079408.
 XX (CROP-) CROPDESIGN NV.
 PA Inze D, De Veylder L, Vlieghe K;
 PI WPI; 2004-348466/32.
 XX P-PSDB; ADN72203.
 DR Altering plant characteristics, useful for producing plants for enzyme or
 PT pharmaceutical production comprises modifying in a plant, expression of
 PT one or more nucleic acids and/or modifying level or activity of one or
 PT more proteins.
 XX Claim 1; SEQ ID NO 97; 134pp; English.
 XX This invention relates to a novel method for altering one or more plant
 CC characteristics. Specifically, it refers to identifying genes that are up
 CC - or down-regulated in transgenic plants overexpressing the heterodimeric
 CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to
 CC alter plant characteristics accordingly. The present invention describes
 CC generating transgenic plants for the production of growth regulators,
 CC enzymes, therapeutics, pharmaceuticals and animal feed products, where
 CC the altered plant characteristics are selected from increased yield or
 CC biomass, enhanced survival capacity, stress tolerance, plant architecture
 CC or physiology, altered endoreduplication, biochemistry, signal
 CC transduction, storage lipid mobilization and/or altered photosynthesis,
 CC each relative to the corresponding wild type plants. Accordingly, these
 CC sequences can also be useful as positive or negative selectable markers
 CC during transformation of cells or tissues. The identified genes play a
 CC role in a variety of biological processes such as DNA replication, cell
 CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as
 CC transcription factors. This polynucleotide sequence is thale cress cDNA
 CC upregulated 1.3 fold or more in plants overexpressing the E2Fa/Dpa
 CC transcription factor, given in an exemplification of the invention.
 XX
 SQ Sequence 630 BP; 191 A; 83 C; 202 G; 154 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.39e-07 Length: 630
 Score: 177.00 Matches: 65
 Percent Similarity: 51.42% Conservative: 44
 Best Local Similarity: 30.66% Mismatches: 73
 Query Match: 16.94% Indels: 30
 DB: 12 Gaps: 13
 US-09-980-758A-8 (1-209) x ADN72202 (1-630)
 QY 16 ArgLysArgGluLeuAlaGluAlaSerSerThrSerPheSerProLeuLysThr 35
 Db 19 AGAGACGAGATGTTGTTGAAGAGATGAGTTACGACG--ACGACGGTGAACACGAGG 75
 QY 36 LysLeuAsnAspSerSerPheSerProAspSerHisAspValPheAlaVal 55
 Db 76 AAGATCGAGGAGGAGTGGAT---TTAGTGAATCTAGGATTAATCTCTCGTGTGTA 132
 QY 56 SerSerSerSer-----ValAlaSerSerAlaAlaLeuAlaSerPheGluCys 71
 Db 133 CAGCGCAGCAATCGCGTGAATTTGGCGAGAAATTCAGCAGGCGTGGAGACGAGT 192
 QY 72 SerValThrIleGlyGlyGluGluSer-----Asp 81
 Db 193 GTTGTTATAGTAGCAGCGCGAGATCTCTCCGGTTGAGAACAGTGTCAATCGAGAA 252
 QY 82 GlnSerSerSerIleSerSerGlyCysPheThrSerGluSerLysGluLeuAlaLysAsn 101

Db 253 GAAGATTCTCGTTCGTTTCGGTGT---TGTTCTATCGAAGAGAAA-----TCGAACCG 303
 QY 102 SerSerSerPheGlyValAspLeuGluAspHisGln---IleGluThrGluThrGluThr 120
 Db 304 AGAATCGAATTT--GTAGATCTTGAGGAAATAACGGTCAGCATCGTGAACAGAAACG 360
 QY 121 SerThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGluGlyLeuGly 140
 Db 361 TCG---TGGATTTACGATGATTTGAATAAG-----AGTCAGGAATCGATGAACATGGAT 411
 QY 141 GluThrThrThrGluMetGluSerSerSerAlaThrLysArgLysGlnProGlyValArg 160
 Db 412 TCTTCTTCGGTGGCTGTTGAAGATGTAGAGTCTCGCCGAGGTTAAGGAAGAGTCTCCAT 471
 QY 161 LysThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAsp 180
 Db 472 GAGACGGTGAAGAAAGCTGAGTTAGAAGACTTTTTTCAGGTGCGCGAGAAA-----GAT 525
 QY 181 LysLysLysGlnPheIleGlu-----LysTyrAsnPheAspIleValAsnAspGlu 197
 Db 526 CTTCGAATAAGTTGTTGGAATGTTCTATGAAGTATACTTCGATTTCGAGAAAGATGAG 585
 QY 198 ProLeu---GluGlyArgTyrLysTyrAspArgLeu 208
 Db 586 CCACTTGGTGGAGGAAGATACGAGTGGTAAATTG 621
 RESULT 11
 AAC85204
 ID AAC85204 standard; DNA; 809 BP.
 AC AAC85204;
 XX 22-MAR-2001 (first entry)
 DE Plant D-like cyclin inhibitor BRO3 coding sequence.
 XX Plant; D-like cyclin inhibitor gene; BRO4; hyperplastic; variant;
 KW growth rate; dividing cells; inactivation; protoplast; seed; root cell;
 XX meristem; leaf; ss.
 OS Arabidopsis thaliana.
 XX
 FH Key Location/Qualifiers
 CDS 69..620
 FT /*tag= a
 FT /product= "BRO3"
 XX WO2000069883-A1.
 XX 23-NOV-2000.
 XX 15-MAY-2000; 2000WO-US013379.
 XX 14-MAY-1999; 99US-0134373P.
 XX (HUTC-) HUTCHINSON CANCER RES CENT FRED.
 XX Roberts J, Kelly B;
 XX WPI; 2001-024998/03.
 XX P-PSDB; AAB47004.
 XX Functionally inactivating expression of plant D-like cyclin inhibitor
 PT gene for producing a hyperplastic variant plant, modulating the growth
 PT and/or yield of plants, and increasing the proportion of dividing cells.
 XX Example 1; Page 39-40; 50pp; English.
 XX The sequence given in AAC85204 represents a plant D1 cyclin inhibitor
 CC gene, BRO3. This sequence was isolated using a yeast two hybrid screen.
 CC The BRO3 protein was found to contain a seven amino acid sequence cyclin
 CC binding domain similar to that of BRO1, BRO2 and BRO4 (See also AAB47005-

6). This sequence is homologous to a sequence present in a D-like cyclin inhibitor gene and when integrated at the corresponding locus, functionally inactivates plant D-like cyclin inhibitor protein expression. The BR04 coding sequence may be used to produce a hyperplastic variant plant, increase the growth rate of a plant, or increase the proportion of dividing cells in a plant cell population, relative to a wild-type plant, by functionally inactivating the expression of a plant D-like cyclin inhibitor gene in a plant. BR04 is useful for increasing the proportion of dividing cells in a plant cell population comprising protoplast, seeds, root cells, meristem cells or leaf cells

XX
SQ Sequence 809 BP; 268 A; 110 C; 213 G; 218 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,928-07 Length: 809
Score: 177.00 Matches: 68
Percent Similarity: 49.12% Conservative: 43
Best Local Similarity: 30.09% Mismatches: 73
Query Match: 16.94% Indels: 42
DB: 5 Gaps: 14

US-09-980-758A-8 (1-209) x AAC85204 (1-809)

QY 2 ArgAspLeuProLysAsnProArgGluLysLysMetSerGluArgLysArgGluLeuAla 21
DB 3 CGAGATTACCA-----CGAGATGCGTT 26

QY 22 GluGluAlaSerSerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSer 41
DB 27 GAAGAGAATGGAGTTACGACG---ACGACGGTGAACGAAGAGATGGAGGAGGAGTG 83

QY 42 AspSerSerProAspSerHisAspValIleValPheAlaValSerSerSerSer----- 59
DB 84 GAT-----TTAGTGAATCTAGGATAATCTCTCGTGTGTACAGCGCAGCAATCGCGT 140

QY 60 -----ValAlaSerSerAlaAlaLeuAlaSerAspGluCysSerValThrIleGlyGly 77
DB 141 GGAATTGTGGGAGAAATTCAGCAGGAGCGTCGGAGACGAGTGTGTTATAGTACGACGG 200

QY 78 GluGluSer-----AspGlnSerSerSerSerSerSerSerSerSerSerSer 87
DB 201 CGAGATTCTCTCCGTTGAAGACAGTGTCAAAATCGAAGAGAGATTCGTCGTTTCG 260

QY 88 SerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSerSerSerPheGlyVal 107
DB 261 TGT-----TGTTCTACATCGAAGAGAAA-----TCGAACGGAGATCGAATTT---GTA 308

QY 108 AspLeuGluAspHisGln---IleGluThrGluThrGluThrSerThrPheIleThrSer 126
DB 309 GATCTTGAGGAAAATAACGGTGACGATCGTGAACACAGAAACGTCG---TGGATTTACGAT 365

QY 127 AsnPheArgLysGluThrSerProValSerGluGlyLeuGlyGluThrThrGluMet 146
DB 366 GATTTGAATAAG-----AGTGAGGAATCGATGGAACATGGATTCCTCTCGTGGCTGTT 419

QY 147 GluSerSerSerAlaThrLysArgLysGlnProGlyValArgLysThrProThrAlaAla 166
DB 420 GAAGATGTAGAGTCTCGCGCAGGTTAAGGAAGAGTCTCCATGACCGGTGAAGAAAGCT 479

QY 167 GluIleGluAspLeuPheSerGluLeuGluSerProAspLysLysLysGlnPheIle 186
DB 480 GAGTTAGAAGACTTTTTCAGGTGCGCGAGAAA-----GATCTTCGGAATAAGTTGTG 533

QY 187 Glu-----LysTyrAsnPheAspIleValAsnAspGluProLeu---GluGlyArg 202
DB 534 GAATGTTCTATGAAGTATAACTTCGATTTTCGAGAAAGATGACCCACTTGGTGGAGGAAGA 593

QY 203 TyrLysTyrAspArgLeu 208
DB 594 TACGAGTGGGTTAAATG 611

RESULT 12

AAD40770
ID AAD40770 standard; cDNA; 861 BP.
AC AAD40770;
XX
DT 30-OCT-2002 (first entry)
XX
DE Arabidopsis thaliana ICK2 full-length cDNA.
XX
KW Plant development; cyclin-dependent kinase; CDK inhibitor; ICK1; ICK2;
KW ICK2; ICK6; ICK7; ICK8; ICKD; morphogenesis; maturation; enlargement;
KW plant breeding; growth; gene; ss.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT CDS 7..636
FT /*tag= a
FT /product= "ICK2 full-length protein"
XX
PN WO200250292-A2.
XX
PD 27-JUN-2002.
XX
PF 18-DEC-2001; 2001WO-CA001825.
XX
PR 18-DEC-2000; 2000US-0255908P.
XX
PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
XX
PI Wang H, Zhou Y, Fowke LC;
XX
XX WPI; 2002-519888/55.
DR P-PSDB; AAE25110.
XX
PT Modifying plant development, e.g. growth or maturation, which is
PT particularly useful in plant breeding, by introducing nucleic acids
PT coding for cyclin-dependent kinase (CDK) inhibitor, cyclin or proteins
PT that bind to CDK inhibitors.
XX
PS Disclosure; Fig 3B; 89pp; English.
XX
CC The invention relates to a method for the development of a plant. The
CC method involves introducing into a plant cell a nucleic acid encoding a
CC protein that binds or interacts with a cyclin-dependent kinase (CDK)
CC inhibitor polypeptide (such as ICK1, ICK2, ICK6, ICK7, ICK8 and
CC ICKD), a cyclin polypeptide, a CDK, or a polypeptide that modulates the
CC degradation of a CDK inhibitor polypeptide. The method is useful for
CC modifying the growth and development of plants e.g. morphogenesis,
CC growth, multiplication, enlargement, differentiation or maturation of a
CC cell or plant. It is particularly useful in plant breeding. The present
CC sequence is A. thaliana ICK2 full-length cDNA
XX
SQ Sequence 861 BP; 266 A; 114 C; 230 G; 251 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,098-07 Length: 861
Score: 177.00 Matches: 65
Percent Similarity: 51.42% Conservative: 44
Best Local Similarity: 30.66% Mismatches: 73
Query Match: 16.94% Indels: 30
DB: 6 Gaps: 13

US-09-980-758A-8 (1-209) x AAD40770 (1-861)

QY 16 ArgLysArgGluLeuAlaGluLysSerSerThrSerPheSerProLeuLysThr 35
DB 25 AGAGAACGAGATGTGTTGAAGAGAAATCGAGTTACGACG---ACGACGGTGAACGAAGG 81

QY 36 LysLeuAsnAspSerSerAspSerProAspSerHisAspValIleValPheAlaVal 55
DB 82 AAGATGGAGGAGGAAGTGGAT---TTAGTGAATCTAGGATAATTTCTCTCCGTTGTGTA 138

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QY 56 SerSerSerSer-----ValAlaSerSerAlaAlaLeuAlaSerAspGluCys 71
DB 139 CAGCGGACGAATCGCGGTGGAATTTGGCGAGAAATTCAGCAGGACGCGTCGAGACGAGT 198
QY 72 SerValThrIleGlyGlyGluGluSer-----Asp 81
DB 199 GTTGTATATAGTACGACGGCGGATCTCTCCGGTTGAAGACAGTGTCMAATCGAAGAA 258
QY 82 GlnSerSerSerIleSerSerGlyCysPheThrSerGluSerLysGluLeuAlaLysAsn 101
DB 259 GAAGATTCTCGGTTTCGTGT---TGTTCTACATCGGAAGAGAAA-----TCGAAACGG 309
QY 102 SerSerSerPheGlyValAspLeuGluAspHisGln---IleGluThrGluThrGluThr 120
DB 310 AGAATCGAATTT---GTAGATCTTGAGGAATAAATACGGTGCAGTCTGTGAAAACAGAAACG 366
QY 121 SerThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGluGlyLeuGly 140
DB 367 TCG---TGGATTTACGATGATTTGATAG-----AGTCAGGAATCGATGAACATGGAT 417
QY 141 GluThrThrThrGluMetGluSerSerSerAlaThrLysArgLysGlnProGlyValArg 160
DB 418 TCTTCTTCGGTGGCTGTTCAAGATGTAGAGTCTCGCCGAGGTAAAGGAAGAGTCTCCAT 477
QY 161 LysThrProThrAlaAlaGluLeuGluAspLeuPheSerGluLeuGluSerProAspAsp 180
DB 478 GAGACGGTGAAGGAAGCTAGTTAGAAAGACTTTTTCAGGTGCGCGAGAAA-----GAT 531
QY 181 LysLysLysGlnPheIleGlu-----LysTyrAsnPheAspIleValAsnAspGlu 197
DB 532 CTTCCGAATAAGTTGTTGGAATGTTCTATGAAGTATTACTTCGATTTTCGAGAAAGATGAG 591
QY 198 ProLeu---GluGlyArgTyrLysTrpAspArgLeu 208
DB 592 CCACCTTGGTGGAGGAAGATACGAGTGGGTAAATTTG 627

RESULT 13
AAC45711
ID AAC45711 standard; DNA; 883 BP.
XX
AC AAC45711;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 47486.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0132863P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
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PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
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PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139500P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
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PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
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Db	693	CCACTTGGTGAGGAGATACGAGTGGTTAAATTG	728
RESULT 14			
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ID	AAC37798	standard; DNA; 886 BP.	
XX			
AC	AAC37798;		
XX			
DT	17-OCT-2000	(first entry)	
XX			
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 18698.		
XX			
KW	Hybridization assay; genetic mapping; gene expression control;		
KW	protein identification; signal transduction pathway; metabolic pathway;		
KW	promoter; termination sequence; ss.		
XX			
OS	Arabidopsis thaliana.		
XX			
PN	EP1033405-A2.		
XX			
PD	06-SEP-2000.		
XX			
PF	25-FEB-2000; 2000EP-00301439.		
XX			
PR	25-FEB-1999;	99US-0121825P.	99US-0139457P.
PR	05-MAR-1999;	99US-0123180P.	99US-0139458P.
PR	09-MAR-1999;	99US-0123548P.	99US-0139459P.
PR	23-MAR-1999;	99US-0125788P.	99US-0139460P.
PR	25-MAR-1999;	99US-0126264P.	99US-0139461P.
PR	29-MAR-1999;	99US-0126785P.	99US-0139462P.
PR	01-APR-1999;	99US-0127462P.	99US-0139463P.
PR	06-APR-1999;	99US-0128234P.	99US-0139750P.
PR	08-APR-1999;	99US-0128714P.	99US-0139763P.
PR	16-APR-1999;	99US-0129845P.	99US-0139817P.
PR	19-APR-1999;	99US-0130077P.	99US-0139899P.
PR	21-APR-1999;	99US-0130449P.	99US-0140353P.
PR	23-APR-1999;	99US-0130510P.	99US-0140354P.
PR	28-APR-1999;	99US-0130891P.	99US-0140355P.
PR	30-APR-1999;	99US-0131449P.	99US-0140695P.
PR	30-APR-1999;	99US-0132048P.	99US-0140823P.
PR	04-MAY-1999;	99US-0132484P.	99US-0140823P.
PR	05-MAY-1999;	99US-0132485P.	99US-0140991P.
PR	06-MAY-1999;	99US-0132486P.	99US-0141287P.
PR	06-MAY-1999;	99US-0132487P.	99US-0141842P.
PR	07-MAY-1999;	99US-0132863P.	99US-0141842P.
PR	11-MAY-1999;	99US-0134256P.	99US-0141842P.
PR	14-MAY-1999;	99US-0134218P.	99US-0141842P.
PR	14-MAY-1999;	99US-0134219P.	99US-0142055P.
PR	14-MAY-1999;	99US-0134221P.	99US-0142055P.
PR	14-MAY-1999;	99US-0134370P.	99US-0142390P.
PR	18-MAY-1999;	99US-0134768P.	99US-0142803P.
PR	19-MAY-1999;	99US-0134941P.	99US-0142920P.
PR	20-MAY-1999;	99US-0135124P.	99US-0142977P.
PR	21-MAY-1999;	99US-0135353P.	99US-0143542P.
PR	24-MAY-1999;	99US-0135629P.	99US-0143624P.
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PR	27-MAY-1999;	99US-0136392P.	99US-0144085P.
PR	28-MAY-1999;	99US-0136782P.	99US-0144086P.
PR	01-JUN-1999;	99US-0137222P.	99US-0144325P.
PR	03-JUN-1999;	99US-0137528P.	99US-0144331P.
PR	04-JUN-1999;	99US-0137502P.	99US-0144332P.
PR	07-JUN-1999;	99US-0137724P.	99US-0144333P.
PR	08-JUN-1999;	99US-0138094P.	99US-0144334P.
PR	10-JUN-1999;	99US-0138540P.	99US-0144335P.
PR	10-JUN-1999;	99US-0138847P.	99US-0144352P.
PR	14-JUN-1999;	99US-0139119P.	99US-0144632P.
PR	16-JUN-1999;	99US-0139452P.	99US-0144814P.
PR	16-JUN-1999;	99US-0139453P.	99US-0145086P.
PR	17-JUN-1999;	99US-0139492P.	99US-0145088P.
PR	18-JUN-1999;	99US-0139454P.	99US-0145088P.
PR	18-JUN-1999;	99US-0139455P.	99US-0145089P.
PR	18-JUN-1999;	99US-0139456P.	99US-0145089P.

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PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154033P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157553P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
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PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0160814P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.
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Alignment Scores:
Pred. No.: 2,166-07
Score: 177.00
Percent Similarity: 51.4%
Best Local Similarity: 30.6%
Query Match: 16.94%
DB: 3

Length: 886
Matches: 65
Conservative: 44
Mismatches: 73
Indels: 30
Gaps: 13

US-09-980-758A-8 (1-209) x AAC37798 (1-886)

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Qy 16 ArgLysArgGluLeuAlaGluAlaSerThrSerPheSerProLeuLysLysThr 35
Db 126 AGAGAACGAGATGTGTTGAGAGAAATGAGTTCAGCG---ACGACGTGAACGAAGG 182
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Qy 36 LysLeuAsnAspSerSerAspSerSerProAspSerHisaspValIleValPheAlaVal 55
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Qy 56 SerSerSerSer-----ValAlaSerSerAlaAlaLeuAlaSerAspGluCys 71
Db 240 CAGCGACGAAATCGCGTGGNAATTCGCGAGAATTCAGCAGGAGCGTCGAGACGAGT 299
Qy 72 SerValThrIleGlyGluGluSer-----Asp 81
Db 300 GTTGTATTAGTACGACGCGAGATTCCTCCGTTGAAGAACAGTGTCAAAATCGAAGAA 359
Qy 82 GlnSerSerSerIleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsn 101
Db 360 GAAGATTCTGCGTTTCGTGT---TGTCTACATCGGAAGAGAAA-----TCGAAACGG 410
Qy 102 SerSerSerPheGlyValAspLeuGluAspHisGln---IleGluThrGluThrGluThr 120
Db 411 AGAATCGAATTT---GTAGATCTTGAGAAATAACCGTGCAGATCGTGAACACGAAACG 467
Qy 121 SerThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGluGlyLeuGly 140
Db 468 TCG---TGATTTACGATGATTTCATAAG-----AGTGAGGAATCGATGAACATGGAT 518
Qy 141 GluThrThrThrGluMetGluSerSerSerAlaThrLysArgLysGlnProGlyValArg 160
Db 519 TCTTCTTCGCTGGCTGTTGAAGATGTAGAGTCTCCGCGCAGGTTAAGGAAGAGTCTCCAT 578
Qy 161 LysThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAsp 180
Db 579 GAGACGCTGAAGGAGCTGAGTTAGAAAGATTTTTCAGGTGGCGGAGAAA-----GAT 632
Qy 181 LysLysLysGlnPheIleGlu-----LysTyrAsnPheAspIleValAsnAspGlu 197
Db 633 CTTCGGAATAAGTTGTTGGAATGTTCTATGAAGTATAACTTCGATTTTCGAGAAAGATGAG 692
Qy 198 ProLeu---GluGlyArgTyrLysTrpAspArgLeu 208
Db 693 CCACTTGTGTGAGGAGAGATACGAGTGGTTAAATTG 728
RESULT 15
AAAX25015
ID AAAX25015 standard; cDNA; 932 BP.
AC AAAX25015;
XX
XX
XX 05-JUL-1999 (first entry)
XX
XX Arabidopsis cyclin-dependent kinase inhibitor FL39 cDNA clone.
XX
XX Cyclin-dependent kinase inhibitor; CDK inhibitor; CKI; CDKI; FL39;
XX plant development; transgenic plant; cell cycle; growth regulator;
XX herbicide, ds.
XX
XX Arabidopsis thaliana.
XX
XX Key Location/Qualifiers
XX CDS 86..715
XX /*tag= a
XX misc_feature 305..932
XX /*tag= c
XX FT polyA_signal 915..920
XX /*tag= b
XX
XX WO9914331-A2.
XX
XX 25-MAR-1999.
XX
XX 16-SEP-1998; 98WO-EP005895.
XX
XX 16-SEP-1997; 97EP-00202838.
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PR 24-DEC-1997; 97EP-00204111.
 XX (CROP-) CROPDISEIGN NV.
 XX Inze D, De Veylder L, De Almeida J, Landrieu I;
 XX WPI; 1999-229535/19.
 XX P-PSDB; AAW98179.
 XX
 XX DNA encoding inhibitor of cyclin-dependent kinase.
 XX
 XX Claim 1b; Page 72-74; 88pp; English.
 XX
 XX This is the DNA sequence of FL39, a cDNA clone that encodes a new cyclin-
 CC dependent kinase (CDK) inhibitor (see AAW98179) of Arabidopsis thaliana.
 CC New plant products with a putative CDK inhibitory function were screened
 CC by using a two-hybrid system with CDC2aAT protein as bait and a library
 CC made from an RNA mixture of A. thaliana cell suspensions harvested at the
 CC early exponential, exponential, early stationary and stationary phases.
 CC Positive clones LDV39, LDV66 and LDV159 were obtained. Clone FL39 was
 CC isolated from a flower cDNA library using partial clone LDV39 as probe.
 CC Clone FL66 (see AAX25016) was similarly obtained using LDV66. Another CDK
 CC inhibitor, ALPCDK1 (see AAX25018), was obtained from alfalfa. Results
 CC established that several CDK inhibitors exist in plants and that these
 CC inhibitors are expressed at different time points and may have different
 CC functions during the development of the plant. CDK inhibitors, nucleic
 CC acids, antibodies, promoter sequences, related recombinant DNA and
 CC vectors are all useful: for diagnosis (no details); for modulating the
 CC cycle, division and/or growth of plant cells; for altering activity of
 CC CDK; for modulating growth inhibition in plants caused by environmental
 CC stress; for inducing male or female sterility; for altering cell division
 CC progression in plants, bacteria, fungi, insect and animal cells; and to
 CC screen for agonists or antagonists that are potentially useful as growth
 CC regulators or herbicides. Plants of any sort can be treated, e.g. to
 CC alter their size or resistance to disease
 XX
 XX Sequence 932 BP; 289 A; 125 C; 254 G; 264 T; 0 U; 0 Other;
 SQ

Alignment Scores:
 Pred. No.: 2.3e-07 Length: 932
 Score: 177.00 Matches: 65
 Percent Similarity: 51.42% Conservative: 44
 Best Local Similarity: 30.66% Mismatches: 73
 Query Match: 16.94% Indels: 30
 DB: 2 Gaps: 13

US-09-980-758A-8 (1-209) x AAX25015 (1-932)

QY 16 ArgLysArgGluLeuAlaGluGluAlaSerSerThrSerPheSerProLeuLysLysThr 35
 DB 104 AGAGAACGAGATCGTGGTGAAGAGAAATGCGAGTTCACGACG---ACGACGGTGAACGAGG 160
 QY 36 LysLeuAsnAspSerSerAspSerProAspSerHisAspValIleValPheAlaVal 55
 DB 161 AAGATGGAGGAGGAAGTGGAT---TTAGTGGAAATCTAGGATAATCTGCTCGGTGTGTA 217
 QY 56 SerSerSerSer-----ValAlaSerSerAlaAlaLeuAlaSerAspGluCys 71
 DB 218 CAGCGCAGCAATCGCGGTGAATTTGGCGAGAAATTCAGCAGGACGTCGGAGACGAGT 277
 QY 72 SerValThrIleGlyGluGluSer-----Asp 81
 DB 278 GTTGTATTATAGTACGCGGCGGAGATTCTCTCCGTTGAAGAACAGTGTCAAAATCGAAGAA 337
 QY 82 GlnSerSerSerIleSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsn 101
 DB 338 GAAGATTCTCGGTGTTCTGGT---TGTTCTACATCGAAGAGAAA-----TCGAAACCG 388
 QY 102 SerSerSerPheGlyValAspLeuGluAspHisGln---IleGluThrGluThrGluThr 120
 DB 389 AGAATCGAATTT---GTAGATCTTGAGGAAATAACGGTCAGCATCGTGAACAGAAACG 445
 QY 121 SerThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGluGlyLeuGly 140

Db 446 TCG---TGGATTACGATGATTTGAATAAG-----AGTGAGGATCGATGAACATGGAT 496
 QY 141 GluThrThrThrGluMetGluSerSerSerAlaThrLysArgLysGlnProGlyValArg 160
 Db 497 TCTTCTTCGGTGGCTGTTGAAGATGTAGAGTCTCGCCGCGAGGTAAAGGAAGAGTCTCCAT 556
 QY 161 LysThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAsp 180
 Db 557 GAGACGGTGAAGAAAGCTGAGTTAGAAGATTTTTTTCAGGTGCGCGAGAAA-----GAT 610
 QY 181 LysLysLysGlnPheIleGlu-----LysTyrAsnPheAspIleValaAsnAspGlu 197
 Db 611 CTTCCGATATAGTTGTTGGATGTTCTATGAAGATATACTTCGATTTCCGAGAAAGATGAG 670
 QY 198 ProLeu---GluGlyArgTyrLysTrpAspArgLeu 208
 Db 671 CCACTTGGTGGAGGAAGATACGAGTGGTGAATTTG 706

Search completed: September 30, 2005, 11:52:35
 Job time : 536 secs

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Qy 16 ArgLysArgGluLeuAlaGluGluAlaSerThrSerPheSerProLeuLysLysThr 35
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Db 104 AGAGAACGAGATGTGGTTGAAGAGAAATGGAGCTTACGACG---ACGCGGTGAACGAACG 161

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Qy 36 LysLeuAsnAspSerSerAspSerSerProAspSerHisAspValIleValPheAlaVal 55
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Db 161 AAGATGGAGGAGGAGTGGAT--TTAGTGGAAATCTAGATAATCTCTCGGTGCTA 217
    |||||
Qy 56 SerSerSerSer-----ValAlaSerSerAlaAlaLeuAlaSerAspGluCys 71
    |||||
Db 218 CAGGCGACGAATCGCGGTGGAAATTTGGCGAGAAATTCAGCAGGAGCGTCGAGACJAGT 277
    |||||
Qy 72 SerValThrIleGlyGlyGluGluSer-----Asp 81
    |||||
Db 278 GTTGTATAGTACGAGCGGAGATCTCTCCGGTTGAAGACATGTCAAATCGAAGAA 337
    |||||
Qy 82 GlnSerSerSerIleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsn 101
    |||||
Db 338 GAAGATTCGTCGTTTCGTGT--TGTTCTACATCGGAAGAGAAA-----TCGAACGG 388
    |||||
Qy 102 SerSerSerPheGlyValAspLeuGluAspHisGln-----IleGluThrGluThrGluThr 120
    |||||
Db 389 AGAATCGAATTT--GTAGATCTTGAGGAAATAACGGGTGACGATCGTGAAACAGAAACG 445
    |||||
Qy 121 SerThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGluGlyLeuGly 140
    |||||
Db 446 TCG--TGAAATTCAGATGATTTGAATAG-----AGTGAGGAATCGATGAACATGGAT 496
    |||||
Qy 141 GluThrThrThrGluMetGluSerSerAlaThrLysArgLysGlnProGlyValArg 160
    |||||
Db 497 TCTTCTCGGTGGCTGTTGAAGATGATAGATCTCCCGCAGGTTAAGGAAGATCTCCAT 556
    |||||
Qy 161 LysThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAsp 180
    |||||
Db 557 GAGACGGTGGAAGAACTGAGTTAGAAGATTTTTCAGGTGGCGGAGAAA-----GAT 610
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Qy 181 LysLysLysGlnPheIleGlu-----LysTyAsnPheAspIleValAsnAspGlu 197
    |||||
Db 611 CTTCCGAATAAGTTGTTGAATGTTCTATGAAGTATAACTTCGATTCGAGAAAGATGAG 670
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Qy 198 ProLeu--GluGlyArgTyrlYsTrpAspArgLeu 208
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Db 671 CCACCTGGTGAGGAGATACGAGTGGGTAAATTG 706
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RESULT 2

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US-09-526-597D-3
; Sequence 3, Application US/09526597D
; Patent No. 6710227
; GENERAL INFORMATION:
; APPLICANT: De Veylder, Lieven
; APPLICANT: De Almeida, Janice
; APPLICANT: Landrieu, Isabelle
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
; FILE REFERENCE: 1187-2
; CURRENT APPLICATION NUMBER: US/09/526,597D
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11)..(658)
US-09-526-597D-3
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Alignment Scores:
Pred. No.: 3.44e-08 Length: 875
Score: 153.00 Matches: 62
Percent Similarity: 42.80% Conservative: 39
Best Local Similarity: 26.27% Mismatches: 73
Query Match: 14.64% Indels: 62
DB: 11 Gaps: 11
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US-09-980-758A-8 (1-209) x US-09-526-597D-3 (1-875)

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Qy 9 ArgGlyLysLysMetSerGluArgLysArgGluLeuAlaGluAlaSerSerThrSer 28
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Qy 29 PheSerProLeuLysLysThrLysLeuAsnAspSerSerAspSerSerProAspSerHis 48
    |||||
Db 65 CCAAGTCCAGGTGTTCCAGAACAGA-----GCCGCT 94
    |||||
Qy 49 AspValIleValPheAlaValSerSerSerValAlaSerSerAlaAlaLeuAlaSer 68
    |||||
Db 95 AAACCCCTAGCTTGAAGCGCTTAATTCCTCCCGCGCTGATTCAGCTCTACCTAACGAC 154
    |||||
Qy 69 AspGluCysSerValThrIleGlyGlyGluGluSerAspGlnSerSerSerIle----- 86
    |||||
Db 155 TCTTCTTGCTATCTTCAGTCCGTAGCGCGCTCTCGAGAAACCCCTCTTCGCTGATTGAA 214
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Qy 87 -----SerSerGlyCysPheThrSerGluSerLysGlu----- 97
    |||||
Db 215 CCGAAACAGCGCCGAGAGTTACAGATCGGGAATTAAGAGTCTGGTTCAGGCTCTCGC 274
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Qy 98 -----IleAlaLysAsnSerSer----- 103
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Db 275 GTTGACTCGGTAACTCGGTTCTCTGAGTCAGAGCTCTAATGAAGATGAATGTTTTCAC 334
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Qy 104 -----SerPheGlyValAspLeuGluAspHisGlnIleGluThrGluThrGluThr 120
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Db 335 AATTTCTGAGTGTCCCAAGTTTCTTGTTGGTGAACAGTCTCGGTTTGAATCAAGACAC 394
    |||||
Qy 121 SerThrPheIleThrSerAsnPheArgLysGluThrSerProValSer-----GluGly 138
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Db 395 AGCACA-----AGGAGAGCAGCGCTTGTAACTTTGTTGAGGAT 433
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Qy 139 Leu-----GlyGluThrThrGluMetGluSerSerSerAlaThr 152
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Db 434 ATGGAGATCATGTTACACAGGCTCTAGCACGAGGTCGATG-----TCGAGAGCAACC 487
    |||||
Qy 153 Lys-----ArgLysGlnProGlyValArgLysThrProThrAlaAlaGluIleGlu 169
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Db 488 AAGAGGTACACAAGGGAACAGATAACGTG-----ATCCGACCACTAGTGAATGGAG 541
    |||||
Qy 170 AspLeuPheSerGluLeuGluSerProAspAspLysLysGlnPheIleGluIleTy 189
    |||||
Db 542 GAGTTCTTTCATATGCAGAG-----CAGCAGCAACAGAGGCTATTTCATCGAGAAATGAC 595
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Qy 190 AsnPheAspIleValAsnAspGluProLeuGluGlyArgTyrlYsTrp 205
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Db 596 AACTTCGACATTGTGAATGATATCCCTCTCAGCGGACGTTACGAATGG 643
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RESULT 3

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US-09-526-597D-5
; Sequence 5, Application US/09526597D
; Patent No. 6710227
; GENERAL INFORMATION:
; APPLICANT: De Veylder, Lieven
; APPLICANT: De Almeida, Janice
; APPLICANT: Landrieu, Isabelle
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
; FILE REFERENCE: 1187-2
; CURRENT APPLICATION NUMBER: US/09/526,597D
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (92)..(763)
US-09-526-597D-5
Alignment Scores:
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Pred. No.: 4.56e-06 Length: 1193
Score: 136.50 Matches: 54
Percent Similarity: 43.04% Conservative: 45
Best Local Similarity: 23.48% Mismatches: 82
Query Match: 13.06% Indels: 49
DB: 4 Gaps: 10

US-09-980-758A-8 (1-209) x US-09-526-597D-5 (1-1193)

QY 11 LysLysMetSerGluArgLysArgGluLeuAlaGluAlaSerSerPheSer 30
DB 116 AAATCCAAATCAGAAATCTCTTCCACCAATTCACCAACACACACACCATCACCATCA 175
QY 31 ProLeuLysThrLysLeuAsnAspSerSerAspSerSerPheSerPheSerHisAspVal 50
DB 176 CCAACCAATCACC---ACCAATTCACCAACCAACCAACCAACCAATCTCTGTGGT 232
QY 51 Ile---ValPheAlaValSerSerSer--- 58
DB 233 GTTCGAACCTCGTGTAGAACCTAGCTTGGAGAAATCCAAATCAGAAATCAGAAATCTT 292
QY 59 SerValalaSerSerAla---AlaLeuAla 67
DB 293 TCTGTTCTTCTGATCTTACCTTACCTCAGTCAGGAACGTCGCTTAAGACACCCCTAATT 352
QY 68 SerAspGluCysSerValThrIleGlyGluSerAspGlnSerSerSerIleSer 87
DB 353 AGCAACATTCCTCCTAAGAGAAATAAGGGCATGATGGAACCTAAATCCCAATT--- 409
QY 88 SerGlyCysPheThrSerGluSerLysGluLeuAlaLysAsnSerSerPheGlyVal 107
DB 410 ---GGGATCAATTGCTGAAGAAACTGTTCAGAGAGCTCCTGAGCCTGAAATGCT 466
QY 108 AspLeuGluAspHisGlnIleGluThrGluThrSerThrPheIleThrSerAsn 127
DB 467 GAATTCAAGCAGAAATGCTGAGGATACTGAGAGAAGCGCT----- 505
QY 128 PheArgLysGluThrSerProVal-----SerGluGlyLeuGlyGlu--- 141
DB 506 ---AGGAAACTACACCGCTCCATTTGATATGCGAGCAGACGCTTCTCAGCGCTCTCT 559
QY 142 ---ThrThrThrGluMetGluSerSerSerAlaThrLysArgLysGlnProGly 158
DB 560 AGCCCAATACAGCGGTACTTTCCAACTGAAGCTAATCCCAAAACGGAGAGCCCACT 619
QY 159 ValArgLysThrProThrAlaAlaGluIleGluAspLysPheSerGluLeuGluSerPro 178
DB 620 ATC-----CCAAATTCACCGCAATTTGAGGAATCTGTCTAAACATGAAGCC--- 667
QY 179 AspAspLysLysLysGlnPheIleGluLysTyAsnPheAspIleValAsnAspGluPro 198
DB 668 ---GAGCAGCAAAAGGAGTTTCATGGAGAAGTACAACCTTGTATCCTGTGACAGAGCCCA 724
QY 199 LeuGluGlyArgTyLysTrpAspArgLeu 208
DB 725 CTCCAGGGCGTTACGAATGGGAAAAGTG 754

RESULT 4

US-09-614-221A-451/c
; Sequence 451, Application US/09614221A
; Patent No. 6723837
; GENERAL INFORMATION:
; APPLICANT: Karunanandaa, Balasulojini
; APPLICANT: Yu, Jaehyuk
; APPLICANT: Kishore, Ganesh M.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
; FILE REFERENCE: 16516.075
; CURRENT APPLICATION NUMBER: US/09/614, 221A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/142, 981
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 626

; SEQ ID NO 451
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-614-221A-451

Alignment Scores:

Pred. No.: 4.76e-06 Length: 612
Score: 132.50 Matches: 61
Percent Similarity: 41.35% Conservative: 25
Best Local Similarity: 29.33% Mismatches: 73
Query Match: 12.68% Indels: 49
DB: 4 Gaps: 9

US-09-980-758A-8 (1-209) x US-09-614-221A-451 (1-612)

QY 7 AsnProArgGluLysLysMetSerGluArgLysArgGluLeuAlaGluAlaSerSer 26
DB 557 AACAGAAGAGTAAAGGCTTCCAAACCAAGCAAGAA---GAAAAGCTAAGGCC 504
QY 27 ThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerAspSerProAsp 46
DB 503 GTCTCTTCTCT---TCCTCCGAATCTTCATCTCA 471
QY 47 SerHisAspValIleValPheAlaValSerSerSerValalaSerSerAlaLeu 66
DB 470 TCT---TCATCTTCATCTGAATCTGAATCTGAGCTGAG 435
QY 67 AlaSerAspGluCysSerValThrIleGlyGluLysArgGlnSerSerSerIle 86
DB 434 TCTGAATCTGAATCTTCATCTTCATCTTCATCTTCATCTTCATCTTCATCT 375
QY 87 SerSerGlyCysPheThrSerGluSer-----LysGluLeuAlaLysAsn 101
DB 374 TCTTCT---GACAGCGAAAGTGAAGCTGAAACCAAGAGGAAGAAATCCAAGAT 324
QY 102 SerSerSerPheGlyValAsp---LeuGluAspHisGlnIleGluThrGluThr 120
DB 323 TCT 264
QY 121 SerThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGluGly 140
DB 263 ACCAAGAAGAGAAATCAAAAGAAATCTTACCTCTGATTCATCTCTCTCTCTCT 204
QY 141 GluThrThrThrGluMetGluSerSerSerSerAlaThrLysArgLysGlnProGlyValArg 160
DB 203 GATAGCGAAAGCGAAAGGAGAGTCTAACGATAAGAAACGTAATCT----- 156
QY 161 LysThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAsp 180
DB 155 ---GAGGACGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 181 LysLysLysGlnPheIleGluLysTyAsnPheAspIleValAsnAspGluPro----- 198
DB 119 AACAGAAGCAAAATAATCAAGAA-----ACCAAGAACCAAGCTACT 78
QY 199 ---LeuGluGlyArgTyLysTrp 205
DB 77 ATTTTCGTTGGTAGACTATCGTG 54

RESULT 5

US-07-667-276A-3
; Sequence 3, Application US/07667276A
; Patent No. 5470971
; GENERAL INFORMATION:
; APPLICANT: Kondo, Keiji
; APPLICANT: Inouye, Masayori
; TITLE OF INVENTION: STRESS-INDUCED PROTEINS, GENES CODING
; TITLE OF INVENTION: THEREFOR, TRANSFORMED CELLS OF ORGANISMS, METHODS AND
; TITLE OF INVENTION: APPLICATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Weiser & Associates

STREET: 230 S. Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/667,276A
FILING DATE: 11-MAR-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 377,5351P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2017 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
STRAIN: S288C
FEATURE:
NAME/KEY: CDS
LOCATION: 484..1725
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1
OTHER INFORMATION: /notes =Base #1 of Sequence No. 5470971 3
OTHER INFORMATION: corresponds to base -483 of the sequence listed in
OTHER INFORMATION: Figure 11 of the application"
US-07-667-276A-3
Alignment Scores:
Pred. No.: 2,97e-05 Length: 2017
Score: 132.50 Matches: 61
Percent Similarity: 41.35% Conservative: 25
Best Local Similarity: 29.33% Mismatches: 73
Query Match: 12.68% Indels: 49
DB: 1 Gaps: 9
US-09-980-758A-8 (1-209) x US-07-667-276A-3 (1-2017)
Qy 7 AsnProArgGluLysLysMetSerGluArgLysArgGluLeuAlaGluAlaSerSer 26
Db 511 AACACGAGGAGTTAAGCTTCCAAACAGCAGCAAGAA-----GAAAAGCTAAGGCC 564
Qy 27 ThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerAspSerProAsp 46
Db 565 GTCTCTTCTCTCT-----TCTCGGAATCTTCATCTCA 597
Qy 47 SerHisAspValIleValPheAlaValSerSerSerValAlaSerSerAlaLeu 66
Db 598 TCT-----TCATCTTCTGAATCTGAATCTGAGTCTGAG 633
Qy 67 AlaSerAspGluCysSerValThrIleGlyGlyGluGluSerAspGlnSerSerIle 86
Db 634 TCTGAATCTGAATCTTCATCTTCATCTTCATCTTCATCTTCATCTTCATCTTCATCG 693
Qy 87 SerSerGlyCysPheThrSerGluSer-----LysGluIleAlaLysAsn 101
Db 877 SerSerGlyCysPheThrSerGluSer-----LysGluIleAlaLysAsn 101

Db 694 TCTTCT-----GACAGCGAAAGTGAAGCTGAAACCAAGAGGAAGATCAAGGAT 744
Qy 102 SerSerPheGlyValAsp---LeuGluAspHisGlnIleGluThrGluThrGluThr 120
Db 745 TCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 804
Qy 121 SerThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGluGlyLeuGly 140
Db 805 ACCAAGAAGGAAGAATCAAAAGAATCTTCTAGCTCTGATTCATCTCATCTTCTTCT 864
Qy 141 GluThrThrThrGluMetGluSerSerSerAlaThrLysArgLysGlnProGlyValArg 160
Db 865 GATAGCGAAGCGAAAGAGAGAGCTTAACGATAGAAACGTAATCT----- 912
Qy 161 LysThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAsp 180
Db 913 -----GAGGACGCCGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 948
Qy 181 LysLysLysGlnPheIleGluLysTyAsnPheAspIleValAsnAspGluPro----- 198
Db 949 AACAAAGAGCAAAAAAATGAAGAA-----ACCGAAGAACCAAGCTACT 990
Qy 199 ---LeuGluGlyArgTyLysTip 205
Db 991 ATTTTCGTTGGTAGACTATCGTGG 1014
RESULT 6
US-09-134-001C-1626
; Sequence 1626, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1626
; LENGTH: 6414
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1626
Alignment Scores:
Pred. No.: 0.000585 Length: 6414
Score: 128.00 Matches: 45
Percent Similarity: 45.45% Conservative: 35
Best Local Similarity: 25.57% Mismatches: 66
Query Match: 12.25% Indels: 30
DB: 3 Gaps: 6
US-09-980-758A-8 (1-209) x US-09-134-001C-1626 (1-6414)
Qy 24 AlaSerSerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSer----- 40
Db 5602 AGCGCAAGTAGCTGATTAAGTGGTCAACAAGTACAGCGAGCTTCAGACTCAACGAGTAGC 5661
Qy 41 -----SerAspSerSerProAspSerHisAspVal 50
Db 5662 TCGACATCAGCAAGTGCATCAACATCAACGAGCGAGCGAGCTCCGATAGCGCAAGTAGC 5721
Qy 51 IleValPheAlaValSerSerSerValAlaSerSerAlaLeuAlaSerAspGlu 70
Db 5722 TCGTTAAGTGGCTCAACAAGATACAGCAATTTTCAGACTCAGAGTAGCTCGACATCAGAC 5781
Qy 71 CysSerValThrIleGlyGlyGluGluSerAspGlnSerSerIleSerSerGlyCys 90
Db 5782 AGTGGTCCACATCCACATCAAGAAAGTGCATCCACATCAACGAGTGTGAGTGATCA--- 5838

Qy	105	PheGlyValAspLeuGluaspHisGlnIleGluThrGluThrGluThrSerThrPheIle	124
Db	754	TCTAGCTCCACAACTCTCCAGTATTCCTGCTACTCAACTGAATATCTCACTGCTCTCA	813
Qy	125	ThrSerAsnPhaArgLysGluThrSerProValserGluGlyLeuGlyGluThr	142
Db	814	AATPACTTCTATTT-----TCATGTAGTCAGCCACGGGGGTGGAGAAACC	855

RESULT 8

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US-09-134-001C-1670/c
; Sequence 1670, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS AUREUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

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RESULT 7

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? PRIOR FILING DATE: 1997-08-14
? NUMBER OF SEQ ID NOS: 5674
? SEQ ID NO 1670
? LENGTH: 783
? TYPE: DNA
? ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1670

```

Alignment Scores:		
Pred. No.:	0.000151	858
Score:	121.50	39
Percent Similarity:	27.83%	Conservative: 27
Best Local Similarity:	48.26%	Mismatches: 61
Query Match:	11.63%	Indels: 11
DB:	4	Gaps: 3

US-09-980-758A-8 (1-209) x US-09-248-796A-8715 (1-858)

60	valalaserseiaalileualaserabpucyserval	431
QY	:	QY
490	AGCGGTCAACGTGACGAAGTGCATCAACATCAACGAGCGTGAGTGACTCCAATAGCGCA	431
Db	:	Db
74	-----ThreileglyGlyGluGluSerAspGlnSerSer 84	
QY	:	QY
430	AGTAGCTCATTAAGTGGCTCAACAAGTACAAAGCGTTTTTCAGACTCAACGAGTACGTGCACA	371
Db	:	Db

Qv 142 ThrThrThrGluMetGluSerSerSerAlaThrLysArgLysGlnProGlyValArgLys 161

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Db 190 AGTACATCGGTAAAGTGAATCATCAAGTACAAGCGTTTCAGATTCA-----ACAAAGT 140
Qy 162 ThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAsp 180
Db 139 ACATCGACATCAGAAAGTGCATCAACGTCACAAAGCGAGTGATCAACAAAGTGAA 83

RESULT 9
US-09-134-001C-1685/c
; Sequence 1685, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1685
; LENGTH: 3561
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1685

Alignment Scores:
Pred. No.: 0.00154 Length: 3561
Score: 121.00 Matches: 51
Percent Similarity: 41.21% Conservative: 31
Best Local Similarity: 25.63% Mismatches: 87
Query Match: 11.58% Indels: 30
DB: 3 Gaps: 4

US-09-980-758A-8 (1-209) x US-09-134-001C-1685 (1-3561)
Qy 9 ArgGluLysLysMetSerGluArgLysArgGluLeuAlaGluLysLys 25
Db 677 AGAGAGAGTGAATCAACAAAGTCAAGTCAAGTCAATGATGAGTGAATCAACAAAGCGTTT 618

Qy 26 -----SerThrSerPheSerProLeuLysLysThrLysLeuAsnAsp 39
Db 617 TCAGATTCAACAAAGTACATCGACATCCGACATCGCTCAACCTCAACAAAGTCAGAGTGAC 558

Qy 40 SerSerAspSerSerProAspSerHisAspValIleValPheAlaValSerSerSer 59
Db 557 TCAAAACAGTGAAGTACATCGTTAAGTGAAGTCAACAAAGCACAAGCGTTTCAGATTCAACA 498

Qy 60 ValAlaSerSerAlaAlaLeuAlaSerAspGluCysSerVal----- 73
Db 497 AGCGGTCAACGTCAAGCAAGTGCATCAACATCAACAGCGTGAGTGACTCCAAATAGCGCA 438

Qy 74 -----ThrIleGlyGlyGluLysSerAspGlnSerSer 84
Db 437 AGTACGTCAATTAAAGTGGCTCAACAAAGTCAACAGCGTTTCAGACTCAACGAGTACGTCACA 378

Qy 85 SerIleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSerSer--- 103
Db 377 TCAGCAAGTGCATCAACATCAACGAGCGAGCGACTCGATAGCGCAAGTACGTCGTTA 318

Qy 104 -----SerPheGlyValAspLeuGluAspHisGlnIleGluThrGluThrSer 121
Db 317 AGTGGCTCAACAAAGTCAACAGCAATTCAGACTCAACAGTACGTCCACATCAGACAGTGGC 258

Qy 122 ThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGluGlyLeuGlyGlu 141
Db 257 TCCATATCCATCAGAAAGTGCATCCACATCAACGAGTGTGAGTGAGTCAGACAGTGAA 198

Qy 142 ThrThrThrGluMetGluSerSerAlaThrLysArgLysGlnProGlyValArgLys 161
Db -----
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Db 197 AGTACATCGGTAAAGTGAATCATCAAGTACAAGCGTTTCAGATTCA-----ACAAAGT 147
Qy 162 ThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAsp 180
Db 146 ACATCGACATCAGAAAGTGCATCAACGTCACAAAGCGAGAGTGATCAACAAAGTGAA 90

RESULT 10
US-09-214-564A-5/c
; Sequence 5, Application US/09214564A
; Patent No. 6150515
; GENERAL INFORMATION:
; APPLICANT: Sharp, Phillip A.
; APPLICANT: Zhou, Qiang
; TITLE OF INVENTION: Tat-SF: Cofactor For Stimulation Of Transcriptional
; FILE REFERENCE: M0656/7042
; CURRENT APPLICATION NUMBER: US/09/214,564A
; CURRENT FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: US 60/021,218
; PRIOR FILING DATE: 1996-07-03
; PRIOR APPLICATION NUMBER: US 60/033,152
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: PCT/US97/11713
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2672
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 58..2319
US-09-214-564A-5

Alignment Scores:
Pred. No.: 0.00252 Length: 2672
Score: 117.50 Matches: 53
Percent Similarity: 44.50% Conservative: 32
Best Local Similarity: 27.75% Mismatches: 85
Query Match: 11.24% Indels: 21
DB: 3 Gaps: 6

US-09-980-758A-8 (1-209) x US-09-214-564A-5 (1-2672)
Qy 4 LeuProLysAsnProArgGluLysLysMetSerGluArgLysArgGluLeuAlaGluGlu 23
Db 2449 CTCCTCAAAACCCACCAAGTCCCTCTCATCAAGATCGTCAACAACTTCTACTGGAA 2190

Qy 24 AlaSerSerThrSer-----PheSerProLeuLysLysThrLysLeuAsnAspSerSer 41
Db 2189 TCTTCTCTCTCATCAACAACTTCTCTCA---TTGGAATCATCATCTTCGACAACTTTTCG 2133

Qy 42 AspSerSerProAspSerHisAspValIleValPheAlaValSerSerSerSerValAla 61
Db 2132 TCAGACTTCTCAACTTCTCTTTTCCA-----TCTGCATCTTCATCTTCCTGTGCA 2085

Qy 62 SerSerAlaAla-----LeuAlaSerAspGluCysSerValThrIleGlyGlyGlu 78
Db 2084 TCTGACTTCTCAACAGCTTTTTCATCTGCATCACTTCTCCGCTTTTTCATCAGCAGCT 2025

Qy 79 GluSerAspGlnSerSerSerIleSerSerGlyCysPheThrSerGluSerLys----- 96
Db 2024 TCAAGCCCTTTTTCATCTGCATATCTTCATCTCTTCTTCATCAGACTCATCAATAAT 1965

Qy 97 -----GluIleAlaLysAsnSerSerPheGlyValAspLeuGluAspHisGlnIle 114
Db 1964 ACTTTTTCATATGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC 1905

Qy 115 GluThrGluThrGluThrSerThrPhe-----IleThrSerAsnPheArgLysGlu 131
Db 1904 TCAGAGCTTCTCTCATCTACACACTTTTTCAGAGCGGTCACTTCAATTCGAGAGTTTCA 1845
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[illegible]

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Qy 132 ThrSerProValSerGluGlyLeuGlyGluThr-----ThrThrGluMetGluSer 148
Db 1844 GAGTCATTTTCTTAACTCTTTTGTCAAGAACATTTTCATGAAGCTCCTTTTCAGAACCT 1785
Qy 149 SerSerAlaThrLysArgLysGlnProGlyValArgLysThrProThrAlaAlaGluIle 168
Db 1784 TCCTCGTCCAAATCTTTCTCGAGACCA---TTTTCTTCAAATCTCTTTCGGAGCCCATCT 1728
Qy 169 GluAspLeuPheSerGluLeuGluSerProAsp 179
Db 1727 TCAGACTGTTTTTCAGAGCAGCTCTTCATCAGAC 1695

RESULT 11
US-09-214-564A-1/c
; Sequence 1, Application US/09214564A
; Patent No. 6150515
; GENERAL INFORMATION:
; APPLICANT: Sharp, Phillip A.
; APPLICANT: Zhou, Qiang
; TITLE OF INVENTION: TAT-SF: Cofactor For Stimulation Of Transcriptional
; TITLE OF INVENTION: Elongation By HIV-1 TAT
; FILE REFERENCE: M0656/7042
; CURRENT APPLICATION NUMBER: US/09/214,564A
; CURRENT FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: US 60/021,218
; PRIOR FILING DATE: 1996-07-03
; PRIOR APPLICATION NUMBER: US 60/033,152
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: PCT/US97/11713
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2815
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 110..2371
; NAME/KEY: unsure
; LOCATION: 46..46
; OTHER INFORMATION: n = a, c, g or t
; NAME/KEY: unsure
; LOCATION: 2731..2731
; OTHER INFORMATION: n = a, c, g or t
US-09-214-564A-1

Alignment Scores:
Pred. No.: 0.00273 Length: 2815
Score: 117.50 Matches: 53
Percent Similarity: 44.50% Conservative: 32
Best Local Similarity: 27.75% Mismatches: 85
Query Match: 11.24% Indels: 21
DB: 3 Gaps: 8

US-09-980-758A-8 (1-209) x US-09-214-564A-1 (1-2815)
Qy 4 LeuProLysAsnProArgGluLysLysMetSerGluArgLysArgGluLeuAlaGluGlu 23
Db 2301 CTCCTCAAAACCAACCCAAAGTCCCTCTCATCAGAACTCGTCAAAACAACACTTCTCACTGGAA 2242
Qy 24 AlaSerSerThrSer-----PheSerProLeuLysLysThrLysLeuAsnAspSer 41
Db 2241 TCTTCTCTCTCATCAACAACACTTCTCA---TTGGAATCATCATCTTCGAAACAACACTTTTCG 2185
Qy 42 AspSerSerProAspSerHisAspValIleValPheAlaValSerSerSerValAla 61
Db 2184 TCAGACTTTCAACTCTCTTTTCCA-----TCTGCATCTTCATCTTCTCTGTCA 2137
Qy 62 SerSerAlaAla-----LeuAlaSerAspGluCysSerValThrIleGlyGlyGlu 78
Db 2136 TCTGACTCTTCAACAGCTTTTTCATCTGTCATCACCTTCTTCGCTTTTATCAGCAGCT 2077

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Db 8145 GATTTCATCATCGTCGCGTCGTCAGACCTCTCTGTCATCGGAGTCGTGGATTTCATCATCG 8086
Qy 85 SerIleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSerSerSer 104
Db 8085 TCGGCGTGTAGATCTCTCATTCGAGTCGTGGAGTCATCATCGTCGCGTCGTCGT 8026
Qy 105 PheGlyValAspLeuGluAspHisGlnIleGluThrGluThrSerThrPheIle 124
Db 8025 -----GATTGCGCGCCAGCCCTCCGAGCGCAGCAGCGATGCTCGACCTCCGCG 7975
Qy 125 ---ThrSerAsnPheArgLysGluThrSer----- 133
Db 7974 AGAATCTCTGCTATTCGCGCGAGCACACAGCTCAGTGAATTCACCTGCGCCACGGACAAT 7915
Qy 134 -----ProValSerGluGlyLeuGluThrSer----- 151
Db 7914 GGCACCGAGGTGACGCCAGGA---GGTTCCGTCGCGGCTCTCTCGTCGCGTCGCGCC 7858
Qy 152 ThrLys-ArgLysGlnProGly-----ValArgLysThrProTh 164
Db 7857 GAGAGGCGCCACACACCGGGGACCGTATCCGCCACCACTGCCACCGCAGACACCGAC 7798
Qy 164 rAlaAla 166
Db 7797 TCCTGCG 7791

RESULT 13

US-09-270-767-1642
; Sequence 1642, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1642
; LENGTH: 938
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-1642

Alignment Scores:
Pred. No.: 0.000661 Length: 938
Score: 116.50 Matches: 49
Percent Similarity: 37.85% Conservative: 32
Best Local Similarity: 22.90% Mismatches: 94
Query Match: 11.15% Indels: 39
DB: 4 Gaps: 6

US-09-980-758A-8 (1-209) x US-09-270-767-1642 (1-938)

Qy 20 LeuAlaGluAlaSerSerThrSerPheSerProLeuLysLysThrLysLeuAsnAsp 39
Db 16 CTGTCCAGTGGATACACACAGATGCAACTACAGTGTCTTCGACAACTGACATC 75
Qy 40 SerSerAspSerSerProAsp----- 46
Db 76 ACCACTGATGGTCAACTGATGAATCCACTGATGGTTCTCTAATGCTCTACTGAGGCG 135
Qy 47 -----SerHisaspValIleValPheAlaValSerSerSerValAla 61
Db 136 TCTACTGAAGCGCGAAGCGAGGACACCAATCTCCACGGAGTCTCCGGATCAACCGAA 195
Qy 62 SerSerAlaAlaLeuAlaSerAspGluCysSerValThrIleGlyGlyGluSerAsp 81
Db 196 AGCACCAGCGCCATCGCCAGTATGGT---TCGACACCGAGGGAAGTACCGTCGAGGAC 252
Qy 82 GlnSerSerSerIleSerSerGlyCysPhe-----ThrSerGlu 94
Db ||||||| |||||||

Db 253 CTGTCGAGTTCCACAAGCTCTGATGTATCTGATTCTTACCATCACGGACTCTCACCT 312
Qy 95 SerLysGluIleAla---LysAsnSerSerSerPheGlyValAspLeuGluAspHisGln 113
Db 313 TCCACTGAGTATCTGGTTCCACAGACTCATCTCTTCCACAGATGGTTCCTCAACAGAT 372
Qy 114 IleGluThrGluThrGluThrSerThrPheIleThrSerAsnPheArgLysGluThrSer 133
Db 373 GCTTCTCCACTGAGGCTTCTCTACCGATGTCTACTGAATCT-----ACAGATAGT 423
Qy 134 ProValSerGluGlyLeuGlyGluThr-----ThrThr 144
Db 424 ACTGTTAGTGGAGTACCGACGACTACCGAAAGCGGTCCACGGAGGAAGTACTACC 483
Qy 145 GluMetGluSerSerAlaThrLysArgLysGlnProGlyValArgLysThrProThr 164
Db 484 GAAGCTCCACTGAAGACACACCGAAGGATCCACACAGCACCACCAATCCACCGATCTG 543
Qy 165 AlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLysLysGln 184
Db 544 GACAGCACCACTGATATCTGGAGCACCACTGATAAGGATGACGAATCGGAGAGCAGT 603
Qy 185 PheIleGluLysTyrAsnPheAspIleValAsnAspGluPro 198
Db 604 ACTCCTTACTCTTTGATTCTGAAGTTACCAAGAGCAAGCCC 645

RESULT 14

US-09-270-767-16924
; Sequence 16924, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16924
; LENGTH: 938
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-16924

Alignment Scores:
Pred. No.: 0.000661 Length: 938
Score: 116.50 Matches: 49
Percent Similarity: 37.85% Conservative: 32
Best Local Similarity: 22.90% Mismatches: 94
Query Match: 11.15% Indels: 39
DB: 4 Gaps: 6

US-09-980-758A-8 (1-209) x US-09-270-767-16924 (1-938)

Qy 20 LeuAlaGluAlaSerSerThrSerPheSerProLeuLysLysThrLysLeuAsnAsp 39
Db 16 CTGTCCAGTGGATGATCAACACAGATGCAACTACAGTGTCTTCGACAACTGACATC 75
Qy 40 SerSerAspSerSerProAsp----- 46
Db 76 ACCACTGATGGTCAACTGATGAATCCACTGATGGTTCTCTAATGCTCTACTGAGGCG 135
Qy 47 -----SerHisaspValIleValPheAlaValSerSerSerValAla 61
Db 136 TCTACTGAAGCGCGAAGCGAGGACACCAATCTCCACGGAGTCTCCGGATCAACCGAA 195
Qy 62 SerSerAlaAlaLeuAlaSerAspGluCysSerValThrIleGlyGlyGluSerAsp 81
Db 196 AGCACCAGCGCCATCGCCAGTATGGT---TCGACACCGAGGGAAGTACCGTCGAGGAC 252
Qy 82 GlnSerSerSerIleSerSerGlyCysPhe-----ThrSerGlu 94
Db ||||||| |||||||

Qy	95	SerLysGluIleAla---	LYaAsnSerSerSerPheGlyValAspLeuGluAspHisGln	113
Db	313	TCCACTGAAGTATCTGGTTCCACAGACTCTCTTCCACAGATGGTTCTTCAACAGAT	372	
Qy	114	IleGluThrGluThrGluThrSerThrPheIleThrSerAsnPheArgLysGluThrSer	133	
Db	373	GCTTCTCCACTGAGGCTTCTCTTACCGATGTCACTGAATCTT-----ACAGATAGT	423	
Qy	134	ProValSerGluGlyLeuGluThr-----ThrThr	144	
Db	424	ACTGTTAGTGGAGGTACACGCGACACTACGGAACGGTCCACCGAGGAAGTACTAC	483	
Qy	145	GluMetGluSerSerAlaThrLysArgLysGlnProGlyValArgLysThrProThr	164	
Db	484	GAAGGCTCCACTGAAAGCACACCGAAGGATCCACAGACAGACGCCCAATCCACCGATCTG	543	
Qy	165	AlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLysLysGln	184	
Db	544	GACAGCACCCACGATGATATCTGGAGCACCAAGTGATGAAGGATGACGAATCGGAGAGCAGT	603	
Qy	185	PheIleGluLysTyrAsnPheAspIleValAsnAspGluPro	198	
Db	604	ACTCCTTACTCTCTTGATTTCTCAAGTTACTCAAGACGAAGCC	645	

[illegible]

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Job time : 192 secs

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OM protein - nucleic search, using frame_plus_p2n model
Run on: September 30, 2005, 11:43:39 ; Search time 656 Seconds
(without alignments)
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Perfect score: 1045
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7442561 seqs, 3452328358 residues
Total number of hits satisfying chosen parameters: 14885122

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-MAXLEN=2000000000 -USR=US09980758 @CGN 1 1 832 @runat_30092005_100633_568
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:
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5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
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9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
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14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:
19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:
20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:
22: /cgn2_6/ptodata/2/pubpna/US10J_PUBCOMB.seq:
23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:
24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1007	96.4	824	9	US-09-733-507-7	Sequence 7, Appli
2	1007	96.4	824	18	US-10-451-139-7	Sequence 7, Appli
3	351.5	33.6	642	9	US-09-733-507-8	Sequence 8, Appli
4	351.5	33.6	642	18	US-10-451-139-8	Sequence 8, Appli
5	213.5	20.4	1040	18	US-10-424-599-69339	Sequence 69339, A
6	181	17.3	904	9	US-09-733-507-1	Sequence 1, Appli
7	181	17.3	904	18	US-10-451-139-1	Sequence 1, Appli
8	177	16.9	861	18	US-10-451-139-18	Sequence 18, Appli
9	177	16.9	932	18	US-10-688-291-1	Sequence 1, Appli
10	174.5	16.7	1261	18	US-10-424-599-67348	Sequence 67348, A
11	174	16.7	660	9	US-09-733-507-3	Sequence 3, Appli
12	174	16.7	660	18	US-10-451-139-3	Sequence 3, Appli
13	172	16.5	1237	18	US-10-424-599-40086	Sequence 40086, A
14	168.5	16.1	804	9	US-09-733-507-15	Sequence 15, Appli
15	168.5	16.1	804	18	US-10-451-139-14	Sequence 14, Appli
16	162.5	15.6	1290	18	US-10-451-139-16	Sequence 16, Appli
17	159	15.2	755	9	US-09-733-507-6	Sequence 6, Appli
18	159	15.2	755	18	US-10-451-139-6	Sequence 6, Appli
19	155	14.8	797	18	US-10-451-139-20	Sequence 20, Appli
20	153.5	14.7	654	21	US-10-890-629-3	Sequence 3, Appli
21	153.5	14.7	1110	18	US-10-425-114-21130	Sequence 21130, A
22	153.5	14.7	1110	20	US-10-425-115-69492	Sequence 69492, A
23	153	14.6	875	18	US-10-688-291-3	Sequence 3, Appli
24	153	14.6	1242	17	US-10-333-006-9	Sequence 9, Appli
25	153	14.6	1671	19	US-10-437-963-18387	Sequence 92632, A
26	151	14.4	906	19	US-10-437-963-18387	Sequence 18387, A
27	151	14.4	1067	17	US-10-333-006-43	Sequence 43, Appli
28	150.5	14.4	533	9	US-09-733-507-9	Sequence 9, Appli
29	150.5	14.4	533	18	US-10-451-139-9	Sequence 9, Appli
30	148.5	14.2	1022	9	US-09-770-443-210	Sequence 210, App
31	148	14.2	642	21	US-10-890-629-1	Sequence 1, Appli
32	148	14.2	1112	18	US-10-425-114-25318	Sequence 25318, A
33	148	14.2	1122	20	US-10-425-115-83466	Sequence 83466, A
34	144	13.8	443	9	US-09-733-507-4	Sequence 4, Appli
35	144	13.8	443	18	US-10-451-139-5	Sequence 5, Appli
36	142	13.6	1360	18	US-10-424-599-92958	Sequence 92958, A
37	139	13.3	377	9	US-09-733-507-5	Sequence 5, Appli
38	139	13.3	377	18	US-10-451-139-4	Sequence 4, Appli
39	138.5	13.3	1183	19	US-10-437-963-96091	Sequence 96091, A
40	138.5	13.3	1721	19	US-10-451-467A-261	Sequence 261, App
41	136.5	13.1	1193	18	US-10-688-291-5	Sequence 5, Appli
42	135.5	13.0	602	19	US-10-767-701-4699	Sequence 4699, Ap
43	134	12.8	765	21	US-10-890-629-11	Sequence 11, Appli
44	134	12.8	1372	9	US-09-993-308-1	Sequence 1, Appli
45	134	12.8	1372	11	US-09-993-808B-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-733-507-7
; Sequence 7, Application US/09733507
; Patent No. US20010025379A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan
; TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth
; TITLE OF INVENTION: Regulators
; FILE REFERENCE: 81601-3
; CURRENT APPLICATION NUMBER: US/09/733,507
; PRIOR FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: CA 2,256,121
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7

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; LENGTH: 824
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-733-507-7

Alignment Scores:
Pred. No.: 2,75e-102 Length: 824
Score: 1007.00 Matches: 202
Percent Similarity: 99.51% Conservative: 0
Best Local Similarity: 99.51% Mismatches: 1
Query Match: 96.36% Indels: 0
DB: 9 Gaps: 0

US-09-980-758A-8 (1-209) x US-09-733-507-7 (1-824)
QY 6 LysAenProArgGluLysMetSerGluArgLysArgGluLeuAlaGluAlaSer 25
DB 28 AAAAAATCCAGAGAGAAAAAATGAGCGAGAGAAAGCGAGAGCTTGCAGAAAGAGCTTCA 87
QY 26 SerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerAspSerPro 45
DB 88 AGCACAGCTTCTCACCAGTCCGCTGAGAGAAACGAGCTTAATGATTCTTCTGATTCATCACG 147
QY 46 AspSerHisAspValIleValPheAlaValSerSerSerValAlaSerSerAlaAla 65
DB 148 GACTCTCATGAGTCATCGTCTTCGCGGTTTTCATCTTCTCCGTTGCTTCGTCGCGGCT 207
QY 66 LeuAlaSerAspGluCysSerValThrIleGlyGlyGluGluSerAspGlnSerSer 85
DB 208 TTAGCGTCTGATGAATGTTCCGTTACCATCGGTGAGAGAAAGTGATCAGTCTCCGAGT 267
QY 86 IleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSerSerPhe 105
DB 268 ATCAGCTCCGTTGTTTCCAGAGTCAATCGAAACCGAAAGAAATCGCGAGTCCGAGT 327
QY 106 GlyValAspLeuGluAspHisGlnIleGluThrGluThrGluThrSerPheIleThr 125
DB 328 GGTGTAGATCTGAGGATCATCAATCGAAACCGAAACCGAAACCTCAACATTCATCAC 387
QY 126 SerAenPheArgLysGluThrSerProValSerGluLysGluLeuGluThrThrGlu 145
DB 388 AGCAATTTTCAGAAAGAGACGAGTCCAGTGAAGTCAAGACGATCAAGAAAGCAATTC 447
QY 146 MetGluSerSerAlaThrLysArgLysGlnProGlyValArgLysThrProThrAla 165
DB 448 ATGGAATTCAGAAAGTACAACTTCGATATTGTCAATGACGAACCGCTTGAAGGTCGCTACAAGTGG 627
QY 206 AspArgLeu 208
DB 628 GATCGACTT 636

RESULT 3
US-09-733-507-8
; Sequence 8, Application US/09733507
; Patent No. US20010025379A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan

; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 7
; LENGTH: 824
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-451-139-7

Alignment Scores:
Pred. No.: 2,75e-102 Length: 824
Score: 1007.00 Matches: 202
Percent Similarity: 99.51% Conservative: 0
Best Local Similarity: 99.51% Mismatches: 1
Query Match: 96.36% Indels: 0
DB: 18 Gaps: 0

US-09-980-758A-8 (1-209) x US-10-451-139-7 (1-824)
QY 6 LysAenProArgGluLysLysMetSerGluArgLysArgGluLeuAlaGluAlaSer 25
DB 28 AAAAAATCCAGAGAGAAAAAATGAGCGAGAGAAAGCGAGAGCTTGCAGAAAGAGCTTCA 87
QY 26 SerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerAspSerPro 45
DB 88 AGCACAGCTTCTCACCAGTCCGCTGAGAGAAACGAGCTTAATGATTCTTCTGATTCATCACG 147
QY 46 AspSerHisAspValIleValPheAlaValSerSerSerValAlaSerSerAlaAla 65
DB 148 GACTCTCATGAGTCATCGTCTTCGCGGTTTTCATCTTCTCCGTTGCTTCGTCGCGGCT 207
QY 66 LeuAlaSerAspGluCysSerValThrIleGlyGlyGluGluSerAspGlnSerSer 85
DB 208 TTAGCGTCTGATGAATGTTCCGTTACCATCGGTGAGAGAAAGTGATCAGTCTCCGAGT 267
QY 86 IleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSerSerPhe 105
DB 268 ATCAGCTCCGTTGTTTCCAGAGTCAATCGAAAGAAATCGCGAGTCCGAGTCCGAGT 327
QY 106 GlyValAspLeuGluAspHisGlnIleGluThrGluThrGluThrSerPheIleThr 125
DB 328 GGTGTAGATCTGAGGATCATCAATCGAAACCGAAACCGAAACCTCAACATTCATCAC 387
QY 126 SerAenPheArgLysGluThrSerProValSerGluLysGluLeuGluThrThrGlu 145
DB 388 AGCAATTTTCAGAAAGAGACGAGTCCAGTGAAGTCAAGACGATCAAGAAAGCAATTC 447
QY 146 MetGluSerSerAlaThrLysArgLysGlnProGlyValArgLysThrProThrAla 165
DB 448 ATGGAATTCAGAAAGTACAACTTCGATATTGTCAATGACGAACCGCTTGAAGGTCGCTACAAGTGG 627
QY 206 AspArgLeu 208
DB 628 GATCGACTT 636

RESULT 2
US-10-451-139-7
; Sequence 7, Application US/10451139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: WANG, HONG
; APPLICANT: ZHOU, YONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
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Qy 197 GluProLeuGluGlyArgTyrIysTrp 205
Db 580 ACGCGCTTGAAGTTCGGTACCAGTGG 606

RESULT 5
US-10-424-599-69339
; Sequence 69339, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 69339
; LENGTH: 1040
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_33625C.1
US-10-424-599-69339

Alignment Scores:
Pred. No.: 115e-13 Length: 1040
Score: 213.50 Matches: 70
Percent Similarity: 48.08% Conservative: 30
Best Local Similarity: 33.65% Mismatches: 67
Query Match: 20.43% Indels: 41
DB: 18 Gaps: 8

US-09-980-758A-8 (1-209) x US-10-424-599-69339 (1-1040)

Qy 11 LysLysMetSerGluArgLysArg-----GluLeuAlaGluAlaSer 25
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Qy 26 SerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerPro 45
Db 115 TCAGCCCAACATTCCTATTCAGAAAGAAAGAAACACCGCTTCC----- 159
Qy 46 AspSerHisAspValIleValPheAlaValSerSerSerValAlaSerSerAla 65
Db 160 -----TTCCAGTTACGCTCTTCCGATACCGAGTTCCTCCGACACT 198
Qy 66 LeuAlaSerAspGluCysSerValThrIleGlyGlyGluGluSerAspGlnSerSer 85
Db 199 ATCGTCTCGCGGAAGCTTCGTTCAGTTCTACCGC-----ACG 237
Qy 86 IleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSerSerPhe 105
Db 238 GTTGTTCGGCGGATTTTGTCTCCATCGC-----TCTTGTCGAGCTCCAGCCAC 288
Qy 106 GlyValAspLeuAlaAspHisGlnIleGluThrGluThrGluThrSerPhe----- 123
Db 289 TTTAAGGACCTC-----CACTCCGTCGCGTCAGATCTGCAGACCAAGGTTTCAACACG 342
Qy 124 -----IleThrSerAsnPheArgLysGluThrSerProValSerGluGlyLeuGly 140
Db 343 GTAGAGGACTCAACCAACCGCTACTTCAAGCGCTTCAGTTGTTGAGTGAGTTTCTGGA 402
Qy 141 GluThrThrThrGluMetGluSerSerAlaThrLysArgLysGlnProGlyValArg 160
Db 403 GACTCGGAGGAATCGCGAAGTCTTCCGCGCAGTCCGGA-----TTG 447
Qy 161 LysThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAsp 180
Db 448 AAGACGCCCAACCAAGCAGATCAAGAGATTTTTCGCGATGGCGGAAAGTACGAG--- 504

Qy 181 LysLysLysGlnPheIleGluLysTyrAsnPheAspIleValAsnAspGluProIleuGlu 200
Db 505 ---CGAAACCGTTTCACAGAGAGTACAACTTTGATATTTGTAGAGATTTCCCGTTGGAG 561

Qy 201 GlyArgTyrLysTrpAspArgLeu 208
Db 562 GGTGCTACCAGTGGTTCGTTTGA 585

RESULT 6
US-09-733-507-1
; Sequence 1, Application US/09733507
; Patent No. US20010025379A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan
; TITLE OF INVENTION: Cyclin Dependand Kinase Inhibitors as Plant Growth
; TITLE OF INVENTION: Regulators
; FILE REFERENCE: 81601-3
; CURRENT APPLICATION NUMBER: US/09/733,507
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: CA 2,256,121
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 904
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (55)..(627)
; NAME/KEY: intron
; LOCATION: (252)..(253)
; NAME/KEY: intron
; LOCATION: (296)..(297)
; NAME/KEY: intron
; LOCATION: (563)..(564)
US-09-733-507-1

Alignment Scores:
Pred. No.: 3.96e-10 Length: 904
Score: 181.00 Matches: 63
Percent Similarity: 42.24% Conservative: 35
Best Local Similarity: 27.16% Mismatches: 68
Query Match: 17.32% Indels: 66
DB: 9 Gaps: 10

US-09-980-758A-8 (1-209) x US-09-733-507-1 (1-904)

Qy 5 ProLysAsnProArgGluLysLysMetSerGluArgLysArgGluLeuAlaGluAla 24
Db 43 CCTAAATCGAAGATGGTCAGAAAATATAGAAAAGCTAAA---GGAATTTGTAGAAGCTGGA 99
Qy 25 SerSerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerAspSerSer 44
Db 100 GTTTTCGTCACGATATATGACGTACGAGCGCGGAGA----- 135
Qy 45 ProAspSerHisAspValIleValPheAlaValSerSerSerSerValAlaSerSerAla 64
Db 136 -----ATTGTTATGTTAGATCGGAAAATCA----- 162
Qy 65 AlaLeuAlaSerAspGluCysSerValThrIleGlyGlyGluGluSerAspGlnSerSer 84
Db 163 -----AGCTCTGCTCTCCGTCGCGTGAT-----AAT 189
Qy 85 SerIleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSerSerSer 104
Db 190 GGAGTTTCGTCGCTCTGT-----AGTGAAGCAATGAATATAAGAGAAAGAAATA--- 240
Qy 105 PheGlyValAspLeuGluAspHisGlnIleGluThrGluThrGluThrSerThrPhe--- 123
Db 241 -----ATACATCTGGAGGAGGAGATAAAGATGTTGACACTGAAACGTCGACGTATCGA 294
Qy 124 -----IleThrSerAsnPheArgLysGlu----- 131

	::: :::	::: :::	::: :::	::: :::
Db	25	AGAGAACGAGATGTGGTTGAACAGAAATCGAGTTCACGACG	---	ACCAGCGGTGAACACGAAGG 81
Qy	36	LysLeuAsnAaspSerSerAaspSerProAaspSerHisAaspValIleValPheAlaVal	55	
Db	82	AAGATCGAGAGAAAGTGAT	---TTAGTGGAACTTAGGATAATTCTGTCCGTGTGTGTA	138
Qy	56	SerSerSerSer-----ValAlaSerSerAlaAlaLeuAlaSerAaspGluCys	71	
Db	139	CAGGCACCAATCGCGGTGGAATTGTGGCGAGAAATTCAGCAGGAGCGTCCGAGACGAGT	198	
Qy	72	SerValThrIleGlyGluGluSer	----	Asp 81
Db	199	GTTGTTATAGTACGACGGCGAGATTCTCTCCGGTTGAAGAACAGTGTCAAATCGAAGAA	258	
Qy	82	GlnSerSerIleSerSerClyCysePheThrSerGluSerLysGluIleAlaLysAsn	101	
Db	259	GAGATTCGTCGGTTCGGT	---TGTCTCATCGGAAGAAAA-----TCGAACCG 309	
Qy	102	SerSerSerPheGlyValAaspLeuGluAspHisGln	---lleGluThrGluThrGluThr 120	
Db	310	AGAAATCGAATTT--GTAGAUCTTGAGGAAAATAACCGTGACGATCTGTGAAAACGAACG	366	
Qy	121	SerThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGluGlyLeuGly	140	
Db	367	TCC--TGCATTTACGATGATTTAAG	-----ACTGAGGAATCGATGAACATGGAT 417	
Qy	141	GluThrThrThrGluMetGluSerSerSerAlaThrLysArgLysGlnProGlyValAsg	160	
Db	418	TCTTCTTCGGTGGCTGTTGAAGATGATAGACTCTCCGCCAGGTTAAGGAAGAGTCTCCAT	477	
Qy	161	LysThrProThrAlaAlaGluIleGluAaspLeuPheSerGluLeuGluSerProAasp	180	
Db	478	GAGACGTCGAAGAAGCTGAGTTAGAACACTTTTTTCAGGTGGCGGAGAAA-----GAT	531	
Qy	181	LysLysGlyGlnPheIleGlu	-----LysTyrAsnPheAaspIleValAasnAaspGlu 197	
Db	532	CTTCGGAATAAGTTGTTGGAATGTTCTATGAAGTATAACTTCGATTTTCGAGAAAGATGAG	591	
Qy	198	ProLeu--GluGlyArgTyrLysTrpAaspArgLeu	208	
Db	592	CCACTTGGTGGAGGAAGATACGAGTGGGTAAATG	627	
RESULT 9				
US-10-688-291-1				
; Sequence 1, Application US/10688291				
; Publication No. US20040073969A1				
; GENERAL INFORMATION:				
; APPLICANT: De Veylder, Lieven				
; APPLICANT: De Almeida, Janice				
; APPLICANT: Landrieu, Isabelle				
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof				
; FILE REFERENCE: 1187-2				
; CURRENT APPLICATION NUMBER: US/10/688,291				
; CURRENT FILING DATE: 2003-10-17				
; PRIOR APPLICATION NUMBER: US/09/526,597D				
; PRIOR FILING DATE: 2000-03-16				
; NUMBER OF SEQ ID NOS: 35				
; SOFTWARE: PatentIn version 3.0				
; SEQ ID NO 1				
; LENGTH: 932				
; TYPE: DNA				
; ORGANISM: Arabidopsis thaliana				
; FEATURE:				
; NAME/KEY: CDS				
; LOCATION: (86)..(712)				
US-10-688-291-1				
Alignment Scores:				
Pred. No.:	1.16e-09	Length:	932	
Score:	177.00	Matches:	65	
Percent Similarity:	51.42%	Conservative:	44	
Best Local Similarity:	30.66%	Mismatches:	73	

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Query Match: 16.94% Indels: 30
DB: 18 Gaps: 13

US-09-980-758A-8 (1-209) x US-10-688-291-1 (1-932)

Qy 16 ArgLysArgGluLeuAlaGluAlaSerSerThrSerPheSerProLeuLysLysThr 35
Db 104 AGAAGACGAGATGTGGTTGAAGAGATGAGTTCACGCG--ACGACGCGTGAACGAGG 160
Qy 36 LysLeuAsnAspSerSerAspSerSerProAspSerHisAspValIleValPheAlaVal 55
Db 161 AAGATGGAGGAGGAAGTGGAT---TTAGTGAATCTAGGATAATTCGTCTCCGTGTGTA 217
Qy 56 SerSerSerSer-----ValAlaSerSerAlaAlaLeuAlaSerAspGluCys 71
Db 218 CAGCGACGAATCCGGTGGAAATTGGCGAGAAATTTCAGCAGGAGCGTCGGAGACGAGT 277
Qy 72 SerValThrIleGlyGlyGluGluSer-----asap 81
Db 278 GTTCTTTATATACGACGCGGAGATTCCTCCGGTTGAAGAACAGTGTCAAATCGAAGAA 337
Qy 82 GlnSerSerIleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsn 101
Db 338 GAAGATTCTGCGGTTTCGTGT---TGTTCTACATCGGAAGAGAAA-----TCGAACCG 388
Qy 102 SerSerSerPheGlyValAspLeuGluAspHisGln---IleGluThrGluThrGluThr 120
Db 389 AGAATCGAATTT---GTAGATCTTTGAGGAAAATAACGGTGACGATCGTGAAACAGAACG 445
Qy 121 SerThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGluGlyLeuGly 140
Db 446 TCG---TCGATTTACGATGATTGAATAAG-----AGTGAGGAATCCGATGAACATGGAT 496
Qy 141 GluThrThrThrGluMetGluSerSerSerAlaThrLysAspLysGlnProGlyValArg 160
Db 497 TCTTCTTCGGTGGCTGTTGAAGATGTAGAGTCTCGCCGACGTTAAGGAAGAGTCTCCAT 556
Qy 161 LysThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAsp 180
Db 557 GAGACGGTGAAGGAAGCTGAGTTAGAGATTTTTTTCAGGTGGCGGAGAAA-----GAT 610
Qy 181 LysLysLysGlnPheIleGlu-----LysTyrAsnPheAspIleValAsnAspGlu 197
Db 611 CTTCCGGAATAAGTTGTTGGAATGTTTATGAAGTATTACTTCGATTTCCGAGAAAGATGAG 670
Qy 198 ProLeu---GluGlyArgTyrLysTrpAspArgLeu 208
Db 671 CCACCTTGGTGAGGAAGATACGATGGGTAAATTTG 706

RESULT 10
US-10-424-599-67348
; Sequence 67348, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 67348
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_3182C.1
US-10-424-599-67348

Alignment Scores:

```

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Pred. No.: 3 35e-09 Length: 1261
Score: 174.50 Matches: 66
Percent Similarity: 47.39% Conservatives: 43
Best Local Similarity: 28.70% Mismatches: 76
Query Match: 16.70% Indels: 46
DB: 18 Gaps: 9

US-09-980-758A-8 (1-209) x US-10-424-599-67348 (1-1261)

QY 12 LysMetSerGluArgLysArgGluLeuAlaGluAlaSerThrSerPheSerPro 31
DB 176 AAGAAGCGAAGCGAAGGAGAACTCGCGCTCGTCAATCCACCAACCAACACCC 235
QY 32 LeuLys-----LysThrLysLeuAsnAspSerSerSerSerPro 45
DB 236 ACCTCTACATGGGGTCCGAACCGCGCCCAAAACCTAGCGCTTCAGAAATCGCAGCG 295
QY 46 AspSerHisAspValIleValPheAlaValSerSerSerSerValAlaSerSerAlaAl 65
DB 296 CAGCAGCAGAGCTC-----GCCGCCACTCCGACTCTACTCTCCAGCTCCGGAGC 346
QY 65 aLeuAlaSer----- 68
DB 347 CGTGGCTCCAGAGGCTCCGATTTGGTCCACTCTCCGAGCGCCCTAAGCACCAGAAC 406
QY 69 ----AspGluCysSerValThrIleGlyGluGluSerAspGlnSerSerIleSe 87
DB 407 CCTAAATCCCAATCCCGAAGCTCCGAGCTCGGACTCGCTTCGAGCGCGAGCTACC 466
QY 87 rSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSer-----Se 103
DB 467 CTCA-----ACCACAACAGAGACAAAT-ACCTTGCATGAGAAATCGCGACCTCAGAG 519
QY 103 rSerPheGly-----ValAspLeuGluAspHisGlnIleGluThrGluThr 120
DB 520 GTCGTTCGGGAAATGTTTGGATTTTCAAGGTAGAGAGAGAGCACTAGGAAATCCAC 579
QY 120 rSerThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGluGlyLeuG 140
DB 580 ACCTTGCAGTTTGTATGAAGGACTCGGATACTGTGCAGGACTCG-----GG 624
QY 140 vGluThrThrThrGluMetGluSerSerSerAlaThrLysArgLysGlnProGlyValAr 160
DB 625 TTCAACTACAGCGCTACTTGTTCAGCTGAAGCTTATCGAAGAACAGACATGCGAGCTAG 684
QY 160 gLys---ThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAs 179
DB 685 AAGCAAAATCCCACTCCCGTGAATGGATGTAATCTTGTGTAATTTGAAGAGGCTCA 744
QY 179 pAspLysLysLysGlnPheIleGluLysTyraenPheAspIleValAsnAspGluProle 199
DB 745 GCAAAAAA-----TTCATTGAGAAGTACAACTTTGATCTCTGCAATGAGAAGCGCT 798
QY 199 uGluGlyArgTyraenPheArgLeu 208
DB 799 CTCAGGCGCTATGAATGGAAAGTTG 826

RESULT 12
US-09-733-507-3
; Sequence 3, Application US/09733507
; Patent No. US2001002579A1
; GENERAL INFORMATION:
; APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: ZHOU, YONGMING
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3

```

```

; LENGTH: 660
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-733-507-3

Alignment Scores:
Pred. No.: 1 54e-09 Length: 660
Score: 174.00 Matches: 52
Percent Similarity: 46.67% Conservatives: 25
Best Local Similarity: 31.52% Mismatches: 48
Query Match: 16.65% Indels: 40
DB: 9 Gaps: 7

US-09-980-758A-8 (1-209) x US-09-733-507-3 (1-660)

QY 72 SerValThrIleGlyGlyGluSerAspGlnSerSerSerIleSerSerGlyCysPhe 91
DB 58 TCTGTCTCGTCTCGTCTCGTCTCGTCTCGTCTCGTCTCGTCTCGTCTCGTCTCGTCT 99
QY 92 ThrSerGluSerLysGluIleAlaLysAsnSerSerSerPheGlyValAspLeuGluAsp 111
DB 100 ---AGTGAAGCAATGCAATATTAAGAAAGAAAGAAATTA-----ATACATCTGGAGGAG 147
QY 112 HisGlnIleGluThrGluThrGluThrSerThrPhe-----Ile 124
DB 148 GAAGATAAAGATGGTGCACACTGAAACGTCGACGTATCGACGGGTACGAGGAAGCTT 207
QY 125 ThrSerAsnPheArgLysGlu----- 131
DB 208 TTTGAAATCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 267
QY 132 -----ThrSerProValSerGluGlyLeu-----GlyGluThrThr 143
DB 268 TCGGAATTTGAATCGCGCTTAAAGAAATCGTTAGATTGTTGTAGCGGAGGAGAAACG 327
QY 144 ThrGluMetGluSerSerSerAlaThrLysArgLysGlnProGlyValArgLysThrPro 163
DB 328 ATGAGAGAGAGCGTACGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 387
QY 164 ThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLysLysLys 183
DB 388 ACGGAATCGGAATTTGAAGATTTTGTGGAAGCTGAGAAA-----CAACTCAAGAGAA 441
QY 184 GlnPheIleGluLysTyraenPheAspIleValAsnAspGluProLeuGluGlyArgTy 203
DB 442 AAATTCAGAAAGAGTACAAATTTTCGATTTCGAGAAAGAGAGAGAGAGAGAGAGAGAG 501
QY 204 LysTyrAspArgLeu 208
DB 502 GAATGGGTAAAGTTA 516

RESULT 12
US-10-451-139-3
; Sequence 3, Application US/10451139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: ZHOU, YONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3

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; LENGTH: 660
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-451-139-3

Alignment Scores:
Pred. No.: 1.54e-09 Length: 660
Score: 174.00 Matches: 52
Percent Similarity: 46.67% Conservative: 25
Best Local Similarity: 31.52% Mismatches: 48
Query Match: 16.65% Indels: 40
DB: 18 Gaps: 7

US-09-980-758A-8 (1-209) x US-10-451-139-3 (1-660)

Qy 72 SerValThrIleGlyGluGluSerAspGlnSerSerSerIleSerSerGlyCysPhe 91
Db 58 TCTGTCCTCCGTCGTCGGTAT-----AATGGAGTTTCGTCTTGT--- 99

Qy 92 ThrSerGluSerLysGluIleAlaLysAsnSerSerPheGlyValAspLeuGluAsp 111
Db 100 ---AGTGAAGCAATATATAAGAAAGAAATTA-----ATACATCTGGAGGAG 147

Qy 112 HisGlnIleGluThrGluThrGluThrSerThrPhe-----Ile 124
Db 148 GAAGATAAAGATGGTGACACTGAACGTCGACGTATCGACGGGTATCGAAGAGGAAGCTT 207

Qy 125 ThrSerAsnPheArgLysGlu----- 131
Db 208 TTTGAAATCTGAGAGAGGAGGAGAAAGAAATTAAGTAATCATCGAGAAATTATTC A 267

Qy 132 -----ThrSerProValSerGluGlyLeu-----GlyGluThrThr 143
Db 268 TCGGAATTGATCGCGCGTTAAAGAAATCGTTAGATTGTTGTAGCGGAGGAAACG 327

Qy 144 ThrGluMetGluSerSerAlaThrLysArgLysGlnProGlyValArgLysThrPro 163
Db 328 ATGGAGGAGACGTCACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 387

Qy 164 ThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLysLys 183
Db 388 ACGGAATCGGAATTTGAAGATTTTTTTGTGGAGCTGAGAAA-----CAACTCAAGAA 441

Qy 184 GlnPheIleGluLysTyrAsnPheAspIleValAsnAspGluProLeuGluGlyArgTyr 203
Db 442 AAATTCAAGAGAAGTACAAATTTCCATTTCGAGAAGGAGAGCCATTAGAAGGCGTTAC 501

Qy 204 LysTrpAspArgLeu 208
Db 502 GAATGGGTAAAGTTA 516

RESULT 13
US-10-424-599-40086
; Sequence 40086, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Zhou Yihua
; APPLICANT: Kovalic David K
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 40086
; LENGTH: 1237
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_136198C.1
US-10-424-599-40086

Alignment Scores:
Pred. No.: 6.2e-09 Length: 1237
Score: 172.00 Matches: 63
Percent Similarity: 48.29% Conservative: 36
Best Local Similarity: 30.73% Mismatches: 74
Query Match: 16.46% Indels: 32
DB: 18 Gaps: 10

US-09-980-758A-8 (1-209) x US-10-424-599-40086 (1-1237)

Qy 20 LeuAlaGluGluAlaSerSerThrSerPheSerProLeuLysLysThrLysLeuAsnAsp 39
Db 318 TTAGCCATGGAAGCTGTAGTTCTGCTGAACCATCATCCAGAGAGAAAGAGATCAGCAAC 377

Qy 40 SerSerAspSerProAspSerHisAspValIleValPheAlaValSerSerSerSer 59
Db 378 AGTACTAACCCAGAGCCAAA-----CTCTCCAGACT 410

Qy 60 ValAlaSerSerAlaAlaLeuAlaSerAspGluCysSerValThrIleGlyGluGlu 79
Db 411 CCGAGAACGAGTCTTCTCTCGCTGTCAAACCCAGCGACGGTGACG-----GAG 458

Qy 80 SerAspGlnSerSer-----IleSerSerGlyCysPheThrSerGluSerLys 96
Db 459 ATGTTTCAGCGCGTGTCTCGCGAGATGTTTCAGCAACGCTGCGCTACCTCCAGT 518

Qy 97 GluIle-----AlaLysAsnSerSerPheGlyValAsp----- 108
Db 519 GAAATTCGGCGCTTCTGCTGCCAGCAACGGATCCATTGGCCTCGATCAGGACAGGATC 578

Qy 109 ---LeuGluAspHisGlnIleGluThr---GluThrGluThrSerThrPheIleThrSer 126
Db 579 AAGCTCTTAGATCGGAGGTGAGCGCGCAAGTTGAAACGTCGACGTGCAATGGTGGT 638

Qy 127 Asn-----PheArgLysGluThrSerProValSerGluGlyLeuGlyGluThrThr 144
Db 639 CATGAAATTCAGAGGAGAGAGATGAAACGTTTCCAGCGAG---CTTCGCGAGAATTCCTCAG 695

Qy 145 GluMetGluSerSerAlaThrLysArgLysGlnProGlyValArgLysThr---Pro 163
Db 696 GAGCGGAGCCAAATGGAGATCAATCTCACCGTCTTTATCAAGGCAAGCCATGCCT 755

Qy 164 ThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLysLys 183
Db 756 ACCGAATTTGGAGCTCGAGGAATTCCTGCTGCCCTCGGAGAAA-----GACATTCAGAAA 809

Qy 184 GlnPheIleGluLysTyrAsnPheAspIleValAsnAspGluProLeuGluGlyArgTyr 203
Db 810 CGATTTCAAGACAGATACAATATGATATTGTTAAGGACGTACCGCTGGAAGGACGCTAC 869

Qy 204 LysTrpAspArgLeu 208
Db 870 GAGTGGGTTCAGTTG 884

RESULT 14
US-09-733-507-15
; Sequence 15, Application US/09733507
; Patent No. US20010025379A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan
; TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth
; TITLE OF INVENTION: Regulators
; FILE REFERENCE: 81601-3
; CURRENT APPLICATION NUMBER: US/09/733,507
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: CA 2,256,121
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 804
; TYPE: DNA

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; ORGANISM: Chenopodium rubrum
US-09-733-507-15

Alignment Scores:
Pred. No.:      8,33e-09      Length:      804
Score:          168.50      Matches:      61
Percent Similarity: 41.67%      Conservative: 34
Best Local Similarity: 26.75%      Mismatches: 66
Query Match:    16.12%      Indels:      67
DB:             9          Gaps:      10

US-09-980-758A-8 (1-209) x US-09-733-507-15 (1-804)

QY 15 GluArgLysArgGluLeuAlaGluAlaSerSerThr---SerPheSerProLeuLys 33
DB 37 GAGCTCGAGACTGCCCTAGCTATGCGCGAGCTGTACTCCAACCTTCGTCTCCGCGGAAG 96
QY 34 LysThrLysLeuAsnAspSerSerAsp----- 42
DB 97 AAGATCAAGAGGTTTCGAGTCTGTATATATCTCAACTAAGAGTCTGCGAAAG 156
QY 43 -----SerSerProAspSerHisAspValIleValPheAlaValSerSerSerVal 60
DB 157 AATTTGTCGCGCGCGAGAT-----TTGCGCGAATTAGAAACGACGCGG 201
QY 61 AlaSerSerAlaAlaLeuAlaSerSerAspGlu-----CysSerValThr 74
DB 202 TTGGAAGTTGCGCGCGTTTTCGAGGAGGAAGAGGTTGCGAATTGCTCGAGTAGCAGGTA 261
QY 75 IleGlyGlyGluGluSerAspGlnSerSerIleSerSerGlyCysPhe----- 91
DB 262 ATTACTACAGTAGTGGAGATTTTCGCGCGTCTGTGCTCAAGCAATTATGATCAGTTG 321
QY 92 ThrSerGluSerLysGluIleAlaLysAsnSerSerPheGlyValAspLeuGluAsp 111
DB 322 AGTTCTAGCGAGCCAGAGTAGCTTAAGGATGATGATGTTTGGGAAATCGTACAGCAGAT 381
QY 112 HisGlnIleGluThrGluThrGluThrSerThrPheIleThrSerAsnPheArgLysGlu 131
DB 382 CCAGAGGTTGAGAGT----- 396
QY 132 ThrSerProValSerGluGlyLeuGlyGluThrThrGluMetGluSerSerSerAla 151
DB 397 -----GTTGAGGCGTCTCAAGCAAAAGTACAAATTCGACATAGTTAAGGACGTG 606
QY 152 ThrLysArgLysGln-----ProGlyValArgLysThr 162
DB 433 ACAGAAGCGAGAGAGCTACAAAATTAGACGACCAGGATTATCCGCGCGAGAAATCAACG 492
QY 163 -----ProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSer 177
DB 493 GTACAGATCAAGATCCGCTGATTTCAGAAATCGAAGAAATCTTTGCTGCTGTAAGAAA 552
QY 178 ProAspAspLysLysLysGlnPheIleGluLysTyrAsnPheAspIleValAsnAspGlu 197
DB 553 -----GATCTCCAGAAACGCTTCAGCGAAAAGTACAAATTCGACATAGTTAAGGACGTG 606
QY 198 ProLeuGluGlyArgTyrLysTyr 205
DB 607 CCACTGAAAGGTCGTATGATTGG 630

RESULT 15
US-10-451-139-14
; Sequence 14, Application US/10451139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: WANG, HONG
; APPLICANT: ZHOU, HONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; APPLICANT: AGRICULTURE AND AGRI FOOD CANADA
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; TITLE OF INVENTION: ACTIVITY

```

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; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 804
; TYPE: DNA
; ORGANISM: Chenopodium rubrum
US-10-451-139-14

Alignment Scores:
Pred. No.:      8,33e-09      Length:      804
Score:          168.50      Matches:      61
Percent Similarity: 41.67%      Conservative: 34
Best Local Similarity: 26.75%      Mismatches: 66
Query Match:    16.12%      Indels:      67
DB:             18          Gaps:      10

US-09-980-758A-8 (1-209) x US-10-451-139-14 (1-804)

QY 15 GluArgLysArgGluLeuAlaGluAlaSerSerThr---SerPheSerProLeuLys 33
DB 37 GAGCTCGAGACTGCCCTAGCTATGCGCGAGCTGTACTCCAACCTTCGTCTCCGCGGAAG 96
QY 34 LysThrLysLeuAsnAspSerSerAsp----- 42
DB 97 AAGATCAAGAGGTTTCGAGTCTGTATATATCTCAACTAAGAGTCTGCGAAAG 156
QY 43 -----SerSerProAspSerHisAspValIleValPheAlaValSerSerSerVal 60
DB 157 AATTTGTCGCGCGCGAGAT-----TTGCGCGAATTAGAAACGACGCGG 201
QY 61 AlaSerSerAlaAlaLeuAlaSerSerAspGlu-----CysSerValThr 74
DB 202 TTGGAAGTTGCGCGCGTTTTCGAGGAGGAAGAGGTTGCGAATTGCTCGAGTAGCAGGTA 261
QY 75 IleGlyGlyGluGluSerAspGlnSerSerIleSerSerGlyCysPhe----- 91
DB 262 ATTACTACAGTAGTGGAGATTTTCGCGCGTCTGTGCTCAAGCAATTATGATCAGTTG 321
QY 92 ThrSerGluSerLysGluIleAlaLysAsnSerSerPheGlyValAspLeuGluAsp 111
DB 322 AGTTCTAGCGAGCCAGAGTAGCTTAAGGATGATGATGTTTGGGAAATCGTACAGCAGAT 381
QY 112 HisGlnIleGluThrGluThrGluThrSerThrPheIleThrSerAsnPheArgLysGlu 131
DB 382 CCAGAGGTTGAGAGT----- 396
QY 132 ThrSerProValSerGluGlyLeuGlyGluThrThrGluMetGluSerSerSerAla 151
DB 397 -----GTTGAGGCGTCTCAAGCAAAAGTACAAATTCGACATAGTTAAGGACGTG 606
QY 152 ThrLysArgLysGln-----ProGlyValArgLysThr 162
DB 433 ACAGAAGCGAGAGAGCTACAAAATTAGACGACCAGGATTATCCGCGCGAGAAATCAACG 492
QY 163 -----ProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSer 177
DB 493 GTACAGATCAAGATCCGCTGATTTCAGAAATCGAAGAAATCTTTGCTGCTGTAAGAAA 552
QY 178 ProAspAspLysLysLysGlnPheIleGluLysTyrAsnPheAspIleValAsnAspGlu 197
DB 553 -----GATCTCCAGAAACGCTTCAGCGAAAAGTACAAATTCGACATAGTTAAGGACGTG 606
QY 198 ProLeuGluGlyArgTyrLysTyr 205
DB 607 CCACTGAAAGGTCGTATGATTGG 630

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Search completed: September 30, 2005, 14:08:48
Job time : 660 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 30, 2005, 11:36:09 ; Search time 3168 Seconds
(without alignments)
2511.184 Million cell updates/sec

Title: US-09-980-758A-8

Perfect score: 1045

Sequence: 1 PDLPKNPREKQMSRKEL.....NFDIVNDFLEGRYKMDRLX 209

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USPTO.spool/US09980758/runat.30092005.100632.520/app.query.fasta.1.391
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0 -L-LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09980758 @CGN.1.1.4352 @runat.30092005.100632.520 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
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2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1007	96.4	797	CNS0A7OL	BX826283 Arabidops
2	991	94.8	893	CNS0A6HI	BX825232 Arabidops
3	923	88.3	664	AU237797	AU237797 Arabidops
4	900	86.1	736	CNS0A6EV	BX826140 Arabidops
5	874	83.6	784	CNS0A6GQ	BX825610 Arabidops
6	492.5	47.1	457	BX840619	BX840619 Arabidops
7	365	34.9	425	AU228889	AU228889 Arabidops
8	306	29.3	654	BZ426940	BZ426940 Arabidops
9	305	29.2	831	BH708120	BH708120 Arabidops

10	298.5	28.6	700	8	BZ083701
11	246	23.5	646	1	AI728644
12	241.5	23.1	794	6	CB288800
13	239	22.9	919	7	CV242992
14	238.5	22.8	888	7	CF212120
15	224	21.4	808	6	CD574460
16	223.5	21.4	902	5	BQ794660
17	223	21.3	672	5	CO098695
18	223	21.3	747	7	CF212022
19	223	21.3	774	7	CF212022
20	222.5	21.3	722	7	CO079309
21	222.5	21.3	815	7	CO079309
22	219	21.0	747	7	CO408371
23	218.5	20.9	712	7	CV234322
24	214.5	20.5	777	7	CO079308
25	214	20.5	817	7	CK934305
26	214	20.5	846	7	CK934861
27	214	20.5	878	6	CD574461
28	209	20.0	815	7	CK934419
29	203	19.4	701	7	CV084380
30	199	19.0	593	7	CN940550
31	193.5	18.5	592	7	CN912198
32	193.5	18.5	945	7	CV280994
33	188	18.0	852	7	CO121570
34	187	17.9	910	7	CV280549
35	186.5	17.8	885	7	CK136404
36	184	17.6	709	5	BU009283
37	183.5	17.6	408	5	BU670981
38	183.5	17.6	707	5	BU62176
39	183	17.5	602	5	BQ863066
40	180	17.2	607	7	CK665094
41	180	17.2	1017	5	BQ481784
42	179	17.1	623	2	BE347049
43	179	17.1	862	7	CV256047
44	178	17.0	569	5	BQ872660
45	177.5	17.0	445	7	CF234588

ALIGNMENTS

CNS0A7OL 737 bp mRNA linear HTC 06-FEB-2004
Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTSL92805 of Silique of strain col-0 of Arabidopsis thaliana
(thale cress).
BX826283.1 GI:42466833
HTC; GSLT cDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 797)
Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation
Unpublished
2 (bases 1 to 797)
Genoscope.
Direct Submission
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,

Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
Genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full_length
<http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis>.

FEATURES

Location/Qualifiers
1..797
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/mol_type="mRNA"
/strain="Col-0"
/db_xref="taxon:3702"
/clone="GSLTSL192805"
/tissue_type="Silique"
/plasmid="pCMVSPORT_6"
complement(1..797)
/gene="At3g19150"

gene

ORIGIN

Alignment Scores:
Pred. No.: 2,12e-96 Length: 797
Score: 1007.00 Matches: 202
Percent Similarity: 99.51% Conservative: 0
Best Local Similarity: 99.51% Mismatches: 1
Query Match: 96.36% Indels: 0
DB: 3 Gaps: 0

US-09-980-758A-8 (1-209) x CNS0A70L (1-797)

QY 6 LysAsnProArgGluLysLysMetSerGluArgLysArgGluLeuAlaGluAlaSer 25
DB 2 AAAAATCCAGAGAGAAAAAATGAGCGAGAGAAAGCGAGCTTGCAGAGAGCTTCA 61
QY 26 SerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerAspSerPro 45
DB 62 AGCACAAGCTCTCACCACTGAAGAAAAACGAAGCTTAATGATTCTCTGATTCAACCG 121
QY 46 AspSerHisAspValIleValPheAlaValSerSerSerSerValAlaSerSerAlaAla 65
DB 122 GACTCTCATGACGTATCGTTCGCGGTTCATCTCTTCGTTCGTTCGCGCGCT 181
QY 66 LeuAlaSerAspGluCySerValThrIleGlyGlyGluGluSerAspGlnSerSerSer 85
DB 182 TTAGCGTCTGATGATGTTCCGTTACCATCGGTGAGAGAAAGTGATCAGTCTCGAGT 241
QY 86 IleSerSerGlyCySerPheThrSerGluSerLysGluIleAlaLysAsnSerSerPhe 105
DB 242 ATCAGCTCCGGTGTTCACCACTGAATCGAAAGAAATCGCGAAGACAGTTCGTCGTT 301
QY 106 GlyValAspLeuGluAspHisGlnIleGluThrGluThrGluThrSerThrPheIleThr 125
DB 302 GGTGTAGATCTGGAGGATCATCAATCGAAACCGAAACCGAAACCTCAACATTCAACACC 361
QY 126 SerAsnPheArgLysGluThrSerProValSerGluGlyLeuGlyGluThrThrGlu 145
DB 362 AGCAATTCAGAAAGAGACGAGTCCAGTCACTGAGGCTTTGGGAGAACGACACAGAA 421
QY 146 MetGluSerSerSerAlaThrLysArgLysGlnProGlyValArgLysThrProThrAla 165
DB 422 ATGGAATCATCATCGCAACCAAGAGAAAAACAACCGCGGGTTCAGGAAGACTCCAAACGCGC 481
QY 166 AlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLysLysGlnPhe 185
DB 482 GCGGAGATTGAGGATTTGTTCTCGGAGCTAGAGATCAAGAGATTAAGAAGAAAGCAATTC 541
QY 186 IleGluLysTrAsnPheAspIleValAsnAspGluProLeuGluGlyArgTyrIleTyr 205
DB 542 ATAGAAAAGTACAACCTTCGATATTCTCAATGACGAACCGCTTGAAGGTCGCTACAAAGTGG 601
QY 206 AspArgLeu 208
|||||

DB 602 GATCGACTT 610

RESULT 2

CNS0A6HI

LOCUS

DEFINITION CNS0A6HI 893 bp mRNA linear HTC 06-FEB-2004
Arabidopsis thaliana Full-length cDNA complete sequence from clone
GSLTSL1212F04 of Silique of strain col-0 of Arabidopsis thaliana
(thale cress).

ACCESSION

VERSION BX825232.1 GI:42465135

KEYWORDS

SOURCE HTC; GSLT cDNA.

ORGANISM

Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eumariophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 893)
Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation

JOURNAL

REFERENCE 2 (bases 1 to 893)

AUTHORS

Genoscope.

TITLE

Direct Submission

JOURNAL

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

COMMENT

The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
Genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full_length
<http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis>.

FEATURES

source

Location/Qualifiers
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/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/strain="Col-0"
/db_xref="taxon:3702"
/clone="GSLTSL1212F04"
/tissue_type="Silique"
/plasmid="pCMVSPORT_6"
complement(1..893)
/gene="At3g19150"

gene

ORIGIN

Alignment Scores:

Pred. No.: 1.24e-94 Length: 893
Score: 991.00 Matches: 199
Percent Similarity: 99.01% Conservative: 2
Best Local Similarity: 98.03% Mismatches: 2
Query Match: 94.83% Indels: 0
DB: 3 Gaps: 0

US-09-980-758A-8 (1-209) x CNS0A6HI (1-893)

QY 6 LysAsnProArgGluLysLysMetSerGluArgLysArgGluLeuAlaGluAlaSer 25
DB 2 AAAAATCCAGAGAGAAAAAATGAGCGAGAGAAAGCGAGCTTGCAGAGAGCTTCA 61
QY 26 SerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerAspSerPro 45
DB 62 AGCACAAGCTTCTCACCACTGAAGAAAAACGAAGCTTAATGATTCTCTGATTCAACCG 121


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QY 46 AspSerHisAspValIleValPheAlaValSerSerSerValAlaSerSerAlaAla 65
|
|
|
Db 122 GACTCTCATGACGTATCGTCTTCGGGGTTTCATCTTCTCGTTCGTTCGGGGCT 181
|
|
|
QY 66 LeuAlaSerAspGluCysSerValThrIleGlyGluGluSerAspGlnSerSer 85
|
|
|
Db 182 TTAGCGTCTGATGAATGTTCCGTTACATCGGTGGAGAGAAAGTATCATGCTCGAGT 241
|
|
|
QY 86 IleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSerSerPhe 105
|
|
|
Db 242 ATCAGCTCCGGTGTGTTTCCACGATGAATCGAAGAAATCGGAAGACAGTTCGTGTT 301
|
|
|
QY 106 GlyValAspLeuGluAspHisGlnIleGluThrGluThrGluThrSerThrPheIleThr 125
|
|
|
Db 302 GGTGTAGATCTGGAGATCATCAATCGAAACCGAAACCGAAACCTCAACATTCATCACC 361
|
|
|
QY 126 SerAsnPheArgLysGluThrSerProValSerGluGlyLeuGlyGluThrThrGlu 145
|
|
|
Db 362 AGCAATTTCCAGAAAGAGACGAGTCCAGTGAGTAAAGGTTTGGAGAAACGACACAGAA 421
|
|
|
QY 146 MetGluSerSerSerAlaThrLysArgLysGlnProGlyValArgLysThrProThrAla 165
|
|
|
Db 422 ATGGAATCATCATCGCAACGAGAGAAACAAACCGGGGTGAGGAAGACTCCCAACGGCG 481
|
|
|
QY 166 AlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLysLysLysGlnPhe 185
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|
|
Db 482 GCGGAGATTTAGGATTTGTTCTCGGAGCTACAGATCAAGACGATAGAAGAACGAAATTC 541
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|
|
QY 186 IleGluLysTyrAsnPheAspIleValAsnAspGluProLeuGluGluValArgTyrLysTrp 205
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|
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Db 542 ATAGAAAAGTACAACTTCGATATTGTAATGACGAACCGCTTGAAGTGCCTACAAGTGG 601
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|
QY 206 AspArgLeu 208
|
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|
Db 602 GATCGACTT 610
|
|
|
```

RESULT 3

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AU237797
LOCUS AU237797 RAFL16 Arabidopsis thaliana cDNA clone RAFL16-57-G19 5',
mRNA sequence. EST 01-APR-2002
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ACCESSION AU237797.1 GI:19876966
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VERSION

```
EST.
```

KEYWORDS

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SOURCE Arabidopsis thaliana (thale cress)
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ORGANISM

```
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
```

REFERENCE

AUTHORS

```
1 (bases 1 to 664)
Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J.,
Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A.,
Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
```

TITLE

JOURNAL

COMMENT

```
Large scale analysis of Arabidopsis full-length cDNA
```

```
Unpublished (2002)
```

```
Contact: Motoaki Seki
```

```
Plant Functional Genomics Research Group
```

```
RIKEN Genomic Sciences Center
```

```
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
```

```
Tel: 81-298-36-4359
```

```
Fax: 81-298-36-9060
```

```
Email: mseki@tc.riken.go.jp
```

```
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda PLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index\_e.html) for further
details.
```

FEATURES

source

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1..664
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/organism="Arabidopsis thaliana"
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/mol_type="mRNA"
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/db_xref="taxon:3702"
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/clone="RAFL16-57-G19"
```

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/lab_host="DH10B"
```

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/clone_lib="RAFL16"
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/note="Site_1: BamHI; Site_2: SalI; dark-grown"
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ORIGIN

Alignment Scores:

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Pred. No.: 1,37e-87 Length: 664
Score: 923.00 Matches: 192
Percent Similarity: 96.06% Conservative: 3
Best Local Similarity: 94.58% Mismatches: 8
Query Match: 88.33% Indels: 1
DB: 1
```

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US-09-980-758A-8 (1-209) x AU237797 (1-664)
```

```
QY 6 LysAsnProArgGluLysLysMetSerGluArgLysArgGluLeuAlaGluAlaSer 25
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|
|
Db 20 AAAAAATCCAGAGAGAAAAAATGACGAGAGAAAGCGAGAGCTTCGAGAAGAGCTTCA 79
|
|
|
QY 26 SerThrSerPheSerProLeuLysThrLysLeuAsnAspSerSerAspSerPro 45
|
|
|
Db 80 AGCACAAAGCTTCTCACCACTGAAGAAACGAAGCTTAATGATTCCTTCTGATTCATCCG 139
|
|
|
QY 46 AspSerHisAspValIleValPheAlaValSerSerSerValAlaSerSerAlaAla 65
|
|
|
Db 140 GACTCTCATGACGTATCGTTCGCGGTTTCATCTTCTCGTTCGTCGGCGCT 199
|
|
|
QY 66 LeuAlaSerAspGluCysSerValThrIleGlyGluGluSerAspGlnSerSer 85
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Db 200 TTAGCGTCTGATCAATGTTCCGTTACCATCGGTGGAGAGAAAGTATCATGCTCTCGAGT 259
|
|
|
```

```
QY 86 IleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSerSerPhe 105
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Db 260 ATCAGCTCCGGTGTGTTCCACGAGTGAATCGAAAGAAATCTCGAAGAACAGTTCGTCGTT 319
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|
|
QY 106 GlyValAspLeuGluAspHisGlnIleGluThrGluThrGluThrSerThrPheIleThr 125
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|
|
Db 320 GGTGTAGATCTGGAGGATCATCAATCGAAACCGAAACCTCAACATTCATCACC 379
|
|
|
QY 126 SerAsnPheArgLysGluThrSerProValSerGluGlyLeuGlyGluThrThrGlu 145
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Db 380 AGCAATTTCCAGAAAAGAGACGAGTCCAGTGAAGGGTTTGGGAGAAAACGACACAGAA 439
|
|
|
QY 146 MetGluSerSerSerAlaThrLysArgLysGlnProGlyValArgLysThrProThrAla 165
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Db 440 ATGGAATCATCATCGCAACGAGAGAAAACACCGGGGGTGAGGAAGACTTCAACGGCG 499
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|
```

```
QY 166 AlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLysLysGlnPhe 185
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Db 500 GCGGAGATTGAGGATTGTTCTCGGAGCTAGAGAGTCAAGACGATNAGAAGAAGCAATTC 559
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QY 186 IleGluLysTyrAsnPheAspIleValAsnAspGluProLeuGluGlyArgTyrLysTrp 205
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|
|
Db 560 NTAGAAAAGTCC-CACCTTCGATATTGNCATATGACCAACCGCTTGAAGGTCGCTCCAGTGGG 618
|
|
|
```

```
QY 206 AspArgLeu 208
|
|
|
Db 619 GATCGACTT 627
|
|
|
```

RESULT 4

CNS0A6EV

LOCUS

DEFINITION

```
CNS0A6EV 736 bp mRNA linear HTC 06-FEB-2004
Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTSL1872B03 of Silique of strain col-0 of Arabidopsis thaliana
(thale cress).
```

ACCESSION

VERSION

KEYWORDS

SOURCE

```
Accession BX826140.1 GI:42465305
Version: HTC; GSLT.cDNA.
Source: Arabidopsis thaliana (thale cress)
```


Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences
A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation

TITLE
JOURNAL
COMMENT

Alignment Scores:
Pred. No.: 2,73e-82 Length: 784
Score: 874.00 Matches: 192
Percent Similarity: 94.74% Conservative: 6
Best Local Similarity: 91.81% Mismatches: 5
Query Match: 93.64% Indels: 6
DB: 3 Gaps: 0

US-09-980-758A-8 (1-209) x CNS0A66Q (1-784)

QY 6 LysAenProArgGluLysMetSerGluArgLysArgGluLeuAlaGluLysSer 25
DB 2 AAAAAATCCAGAGAGAAAAAATGACGAGATATAAGCGAGAGCTTGCAGAGAAAGCTTCA 61
QY 26 SerThrSerPheSerProLeuLysThrLysLeuAenAspSerSerAspSerPro 45
DB 62 AGCAGAGCTTCTCCACCTGAGAAACGAGCTTAATGATTTCTTGATTCATCCG 121
QY 46 AspSerHisAspValIleValPheAlaVal-SerSerSerValAlaSerSerAlaAl 65
DB 122 GACTCTCATTCATGTCATGCTTCGCGGTTTTCATCTTCTTCGTCGTCGCGGC 181
QY 65 aleuAlaSerAspGluCysSerValThrIleGlyGluGluSerAspGlnSerSerSe 85
DB 182 TTTAGCATCTGATGAATGTTCCGTTTACCATCGGTGGAGAGAAAGTGATCAGTCTCCGAG 241
QY 85 rleSerSer-GlyCysPheThr-SerGluSerLysGluIleAlaLysAenSerSer 104
DB 242 TATCAGCTCGCGGTTGTTTCACCGAGTAAATCGAAAGAAATCGCGAAGATCAGTTCGTCG 301
QY 105 PheGlyValAspLeuGluAspHisGlnIleGluThrGluThrGluThr-SerThrPheIl 124
DB 302 TTTGGTGTAGATCTGGAGATCATCAATCGAACCGAAACCGAAGCTCAACATTCAT 361
QY 124 eThrSerAenPheArgLysGluThrSerProValSerGluGlyLeuGlyGluThrTh 144
DB 362 CACAGCAATTTTCAGAAAAGACAGCAGTCCAGTCCAGTGGGGGTTGGGAGAAACCAAC 421
QY 144 rGluMetGlu-SerSerSerAla-ThrLysArgLysGlnProGlyValArgLysThrPro 163
DB 422 AGAATAGGAATCATCATCGGCAACGAGAGAGAAACACCGGGGGGTGAGGAATACTCCA 481
QY 164 ThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLysLys 183
DB 482 ACAGCGCGGAGATGAGATTTGTTCTCGAGCTTAAGAGTCAAGCATAGAGAGAG 541
QY 184 GlnPheIleGluLysTyraPheAspIleValAenAspGluProLeuGluGlyArgTyr 203
DB 542 CAATTATAGAAAGTACAACTTCGATATTGTCAATGACGAACCGCTTAAAGGTCCCTAC 601
QY 204 LysTrpAspArgLeu 208
DB 602 AAGTCGGATCGACTT 616

RESULT 6
EX840619
LOCUS
DEFINITION
Arabidopsis thaliana Silique Col-0 Arabidopsis thaliana
cDNA clone GSLTSL172H03 5PRIM, mRNA sequence.
ACCESSION
BX840619
VERSION
BX840619.1
KEYWORDS
EST, GI:42534702
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 457)
Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M.

REFERENCE
AUTHORS

Alignment Scores:
Pred. No.: 4,1e-42 Length: 457
Score: 492.50 Matches: 120
Percent Similarity: 84.77% Conservative: 8
Best Local Similarity: 79.47% Mismatches: 17
Query Match: 47.13% Indels: 9
DB: 5 Gaps: 2

US-09-980-758A-8 (1-209) x BX840619 (1-457)

QY 11 LysLysMetSerGluArgLysArgGluLeuAlaGluLysSerThrSerPheSer 30
DB 2 AAAAAATGAGCGAGAGAAAGCGAGAGTT-TCAGAGAAAGCTTCAAGCAAGCTTCTCA 60
QY 31 ProLeuLysLysThrLysLeuAenAspSerSerSerSerProAspSerHisAspVal 50
DB 61 CCACCTGAGAAACCAAGCTTAATGATTTCTGATTCATCCGAGTCTCATGACGTC 120
QY 51 IleValPheAlaValSerSerSerValAlaSerSerAlaAlaLeuAlaSerAspGlu 70
DB 121 ATCGCTTCGCGGTTTCATCTTCTCCGTTGCTCGCGGCTTTAGCGTCTGATGAA 180
QY 71 CysSerValThrIleGlyGlyGluSerAspGlnSerSerSerIleSerSerGlyCys 90
DB 181 TGTTCGTTTACCATCGGTGAGAGAAAGTATCAGTCTCGAGTATCAGCTCCGTTGT 240
QY 91 PheThrSerGluSerLysGluIleAlaLysAenSerSerPheGlyValAspLeuGlu 110
DB 241 TTCACGAGTGAATCGAAAGAAATCGGAAGAACAGTTCGTGTTATGTGTAGATCTCGA 300
QY 110 uAspHisGlnIleGluThrGluThrSerThrPheIleThr-----SerAsnPh 128
DB 301 GGATCATATAAATCAAAACCGAAAGAAAG-ACTACAACATTCACACACGCGAATCTT 359
QY 128 eArgLysGluThrSerProValSerGlu-----GlyLeuGlyGluThrThrGlu 145
DB 360 CAGAAAAGAGACAGAGATT-CCAAGTGTAGTGGGATAGGATGAACACGACACACGAA 418
QY 145 uMetGluSerSerSerAlaThrLysArgLys 155
DB 419 ATGCGAACTCACTTCATTCGCGCAACGAAAG 449

FEATURES
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/organism="Arabidopsis thaliana"
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/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="GSLTSL172H03"
/tissue_type="Silique"
/clone_lib="Arabidopsis thaliana Silique Col-0"

ORIGIN

RESULT 7	AU228889	425 bp	mRNA	linear	EST 23-APR-2002			
LOCUS	AU228889	425 bp	mRNA	linear	EST 23-APR-2002			
DEFINITION	Arabidopsis thaliana cDNA clone RAFL16-57-G19 3', mRNA sequence.							
ACCESSION	AU228889	GI:19743536						
VERSION	AU228889	EST						
KEYWORDS	Arabidopsis thaliana (thale cress)							
SOURCE	Arabidopsis thaliana							
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.							
REFERENCE	1 (bases 1 to 425)							
AUTHORS	Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.							
TITLE	Large scale analysis of Arabidopsis full-length cDNA							
JOURNAL	Unpublished (2002)							
COMMENT	Contact: Motoaki Seki Plant Functional Genomics Research Group RIKEN Genomic Sciences Center 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan Tel: 81-298-36-4359 Fax: 81-298-36-9060 Email: mseki@rtc.riken.go.jp An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.							
FEATURES	Location/Qualifiers							
source	1..425							
	/organism="Arabidopsis thaliana"							
	/mol_type="mRNA"							
	/db_xref="taxon:3702"							
	/clone="RAFL16-57-G19"							
	/lab_host="DH10B"							
	/clone_lib="RAFL16"							
	/note="Site_1: BamHI; Site_2: SalI; dark-grown"							
ORIGIN								
Alignment Scores:								
Pred. No.:	1..27e-28	Length:	425					
Score:	365.00	Matches:	76					
Percent Similarity:	95.06%	Conservative:	1					
Best Local Similarity:	93.83%	Mismatches:	2					
Query Match:	34.93%	Indels:	2					
DB:	1	Gaps:	0					
US-09-980-758A-8 (1-209) x AU228889 (1-425)								
QY	130	LysGluThrSerProValSerGluGlyLeuGlyGluThrThrGluMetGluSerSer	149					
DB	424	AAAGAGACGAGTCCATTGAGTCGAGGTTGGGAGAAACGACACAGAAATGGAATCATCA	365					
QY	150	SerAlaThrLysArgLysGlnProGlyValArgLysThrProThrAla-alaGluIleG1	169					
DB	364	TCGGCAACGAAGAGAAACACCGGGGTGAGGAAGACTCCAAACGGCGGGGAGATTGA	305					
QY	169	uAspLeuPheSerGluLeuGluSerProAspAspLysLysLysGlnPheIleGluLysTy	189					
DB	304	GGATTGTGTTCTCGAGCTAGAGAGTCAAGACGATAAGAAGAAGCAATTCATAGAAAAGTA	245					
QY	189	rAsnPheAspIleValAsnAspGluProLeuGluGlyArgTyrLys-TripAspArgLeu	208					
DB	244	CAACTTCGATATGTGTAATGACGAACCGCTGGAAGTCCCTACAAAGGTGGATCGACTT	186					
RESULT 8	BZ426940	654 bp	DNA	linear	GSS 13-DEC-2000			
LOCUS	BONIN07TR BO_1.6.2_KB_tot	654 bp	DNA	linear	GSS 13-DEC-2000			
DEFINITION	genomic survey sequence.							
ACCESSION	BZ426940	GI:26668452						
VERSION	BZ426940.1	GSS						
KEYWORDS	Brassicaceae							
SOURCE	Brassicaceae							
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.							
REFERENCE	1 (bases 1 to 654)							
AUTHORS	Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.							
TITLE	Whole genome shotgun sequencing of Brassica oleracea							
JOURNAL	Unpublished (2001)							
COMMENT	Other_GSSs: BONIN07TF Contact: Chris Town TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523 Fax: 301-838-0208 Email: cdtown@tigr.org DNA is from a doubled haploid provided by Tom Osborn. Seq primer: TR Class: sheared ends.							
FEATURES	Location/Qualifiers							

```

Db      339 ATGACTCAATCTGTGAATCTTCATTGATTTCTTCCTTCGTTTGTGTTTCAGACTCAT 398
Qy      113 GlnileGluThrGluThrGluThrSerThrPheilleThrSerAsnPheArglyGluThr 132
Db      399 CAAATCTCCGATGATCTCTCTCTGTTCTGGCGCATC-----TCTCACAGAAACGAGGCG 452
Qy      133 SerProValSerGluLeuGluThrThrGluMetGluSerSerSerAlaThr 152
Db      453 AATCCAGCGAGTGAAGCTTTGGAGAG---ACAACAGAGTTTGAATCATCATCGCGGTA 509
Qy      153 LysArg-----LysGlnProGlyValArgLysThrProThrAlaAlaGluille 168
Db      510 GAGAGGATGATCGGAAAGTTCACCGGAAGTGAGCAAGATCCGACGCGCGGAGATT 569
Qy      169 GluAppLeuPheSerGluLeuGluSerProAspAspLysLysGlnPheilleGluLys 188
Db      570 GAGGAGTTCTTATCGAGCTAGAGTAATAAGAT-----CAGAAGCGTTTCATGATAAG 623

RESULT 9
BH708120      831 bp      DNA      linear      GSS 20-FEB-2002
LOCUS      BOHYL71TF BO_2.3_KB Brassica oleracea genomic clone BOHYL71,
DEFINITION      genomic survey sequence.
ACCESSION      BH708120
VERSION      BH708120.1 GI:18793934
KEYWORDS      GSS.
SOURCE      Brassica oleracea
ORGANISM      Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 831)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other GSSs: BOHYL71TR
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
FEATURES
Location/Qualifiers
1..831
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strains="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOHYL71"
/clone_lib="BO_2.3_KB"
/note="Vector: pHOE1; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOE1 using BstXI linkers"
ORIGIN
Alignment Scores:
Pred. No.: 7 45e-22 Length: 831
Score: 305.00 Matches: 98
Percent Similarity: 49.00% Conservative: 24
Best Local Similarity: 39.36% Mismatches: 56
Query Match: 29.19% Indels: 72
DB: 8 Gaps: 11

US-09-980-758A-8 (1-209) x BH708120 (1-831)
Qy      2 ArgAspLeuProLysAsnProArgGluLysLys-----MetSerGluArg---- 16
Db      119 AGAGAGCAAAAAAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 178
Qy      17 -----LysArgGluLeu---AlaGluGluAlaSerSerThrSerPheSerProLeu 32

```

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Db      179 CCTAACTGCAAGCGTGATCGCGAGCGGCTTGAAGCTCCGAGCGCAAGCGACTCGCAACTC 238
Qy      33 LysLysThrLysLeuAsnAspSerSerAspSerSerProAspSerHisAspValileVal 52
Db      239 AAGAAGAAGAAGCTCGATGAT-----GACTCTCATGCGTCGTCCTTC 280
Qy      53 PheAlaValSerSerSerValAlaSerSerAlaAlaLeuAlaSerAspGluCysSer 72
Db      281 CTCGCGGTTCTCTCTTCCTTCCTTCGATCGATGATTCCTCTCGAGCGGATGCTCT 340
Qy      73 ValThrIleGlyGluGluSerAspGlnSerSerSerIleSerSerGlyCysPheThr 92
Db      341 GTTACTCCGCGGAGAGACGATGACAGAGCTCGATCATC-----TGTTCAGC 391
Qy      93 SerGluSerLysGluIleAlaLysAsnSerSerPheGlyValAspLeuGlu----- 110
Db      392 AGTGAATCGAACAAATCCGAGGAAGAGTCCGACTGTTTCTGTAGATCTGGAGGTGAGA 451
Qy      110 ----- 110
Db      452 TTTTTCGAAATCAGAGCTCGTCTCTGTTTGAACAATCATTCGATGACTCAATCTCTGT 511
Qy      111 -----AspHisGlnIleGluThrGlu 117
Db      512 GAATCTTCATTGATTTCTTTCCGTTTGTGTGTCAGACTCATCAATCTCCGATGAT 571
Qy      118 ThrGluThrSerThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGlu 137
Db      572 CTCTCTGTTCTGGCGCATC-----TCTCACAGAAACGAGCGGAATCCAGCGAGTGAA 625
Qy      138 GlyLeuGlyGluThrThrGluMetGluSerSerSerAlaThrLysArg----- 154
Db      626 GCTTTGGGAGAG---ACAACAGAGTTGGAATCATCATCGCGGTAGAGAGGATGATCGG 682
Qy      155 ---LysGlnProGlyValArgLysThrProThrAlaAlaGluIleGluAspLeuPheSer 173
Db      683 AAAAGTTACCGGAAGTGAGCAAGATCCGACGCCGCGGAGATTGAGGAGTCTTATCG 742
Qy      174 GluLeuGluSerProAspAspLysLysGlnPheilleGluLys----- 188
Db      743 GAGCTAGAGAT-AAAGAT-----CAGAAGCGTTTTCATGATAAGTGAAGTCTCATCTCCG 795
Qy      189 -----TyrAsnPheAspIle 193
Db      796 ATCTCTTCTCTCTTAATTTTCTCTC 822

RESULT 10
BH083701      700 bp      DNA      linear      GSS 10-OCT-2002
LOCUS      lKx95all.g1 B.oleracea002 Brassica oleracea genomic, genomic survey
DEFINITION      sequence.
ACCESSION      BH083701
VERSION      BH083701.1 GI:23712611
KEYWORDS      GSS.
SOURCE      Brassica oleracea
ORGANISM      Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 700)
Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
Nash,W., Rabinowicz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: lKx95 row: a column: 11
Seq primer: -28RPOT reverse
Class: shotgun
High quality sequence start: 64
High quality sequence stop: 551.

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FEATURES
  source
    Location/Qualifiers
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        /organism="Brassica oleracea"
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        /db_xref="taxon:3712"
        /clone_lib="B.oleracea002"
        /note="Vector: pOTw13; Whole genome shotgun library from
        flowering buds. DNA was purified from a crude nuclear
        prep using Brassica oleracea TO1000DH3 buds. Provided by
        Thomas Osborn at the University of Wisconsin. Genomic
        DNA was provided by Pablo Rabinowicz (CSHL) and the
        shotgun library prepared at Washington University Genome
        Sequencing Center."
ORIGIN
Alignment Scores:
Pred. No.:      2,896-21      Length:      700
Score:          298.50      Matches:      88
Percent Similarity: 49.11%      Conservative: 22
Best Local Similarity: 39.29%      Mismatches:  51
Query Match:    28.56%      Indels:      63
DB:             8           Gaps:        9
US-09-980-758A-8 (1-209) x BZ083701 (1-700)
Qy  17 LysArgGluLeuAlaGlu---GluAlaSerThrSerPheSerProLeuLysLysThr 35
Db  44 AAGCGTACTACAGAAAGCTTGAGCTCCGAGCGCAAGCACTCCCACTCAGAGAGAG 103
Qy  36 LysLeuAsnAspSerSerAspSerSerProAspSerHisAspValIleValPheAlaVal 55
Db  104 AAGTCGATGAT-----GACTCTCATGGCGTCTCTCTCGCGGT 145
Qy  56 SerSerSerSerValAlaSerSerAlaAlaLeuAlaSerAspGluCysSerValThrIle 75
Db  146 CTTTCTCCTCCGTGGCTTCATCGGATGATTCCTCGAGCGGATGCTCTGTACCTCC 205
Qy  76 GlyGlyGluGluSerAspGlnSerSerIleSerSerGlyCysPheThrSerGluSer 95
Db  206 GCCGAGAGAGCATGACAGAGCTCGATCATC-----TGTTTCAGAGTGAATCG 256
Qy  96 LysGluIleAlaLysAsnSerSerPheGlyValAspLeuGlu-----110
Db  257 AACGAAATCCCGAGGAGAGTCCGACTCTTTCTGTAGATCTGGAGGTGAGATTTTCGAA 316
Qy  110 -----110
Db  317 AATCAGAGCTGCTCTCTGTTTGAACAATCATTCGATGACTCAAAATCTGGAATCTTCA 376
Qy  111 -----AspHisGlnIleGluThrGluThrGluThr 120
Db  377 TTGATTTCTTTCCGTTTGTGTTGTCAGACTCATCAAACTCCGATGATCTCTCTGTT 436
Qy  121 SerThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGluLeuGly 140
Db  437 TCTGGCGCATC-----TCTCACAGAAACGAGGCGAATCCAGCGAGTGAAGCTTTGGGA 490
Qy  141 GluThrThrThrGluMetGluSerSerSerAlaThrLysArg-----LysGln 156
Db  491 GAG---ACAACAGAGTTTGGAAATCATCATCGCGGTAGAGAGGGATGATCGGAAAGTTCA 547
Qy  157 ProGlyValArgLysThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGlu 176
Db  548 CCGNAGTGACCAAGAATCCGACGCCGCGGAGATGAGGATTTCTTATCGAGCTAGAG 607
Qy  177 SerProAspAspLysLysGlnPheIleGluLys-----188
Db  608 AATAAGAT-----CAGAAGCGTTTCATGGATAAGTCAGTCTCATCTCCGATCTCTTCT 661
Qy  189 ---TyrAsnPhe 191
Db  662 TCCTTTAATTTT 673
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RESULT 11
AI728644
LOCUS
DEFINITION
  AI728644
  646 bp mRNA linear EST 11-JUN-1999
  to (AJ0021173) Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar
  [Chenopodium rubrum], mRNA sequence.
ACCESSION
  AI728644
VERSION
  AI728644.1 GI:5047496
KEYWORDS
  EST.
SOURCE
  Gossypium hirsutum (upland cotton)
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE
  1 (bases 1 to 646)
  Blewitt, M., Matz, E.C., Davy, D.F. and Burr, B.
  ESTs from developing cotton fiber
  Unpublished (1999)
  JOURNAL
  Contact: Ben Burr
  COMMENT
  Biology Department
  Brookhaven National Laboratory
  Upton, NY 11973 USA
  Tel: 516-344-3396
  Fax: 516-344-3407
  Email: burr@bnl.bnl.gov
  Seq primer: T3 Primer.
  Location/Qualifiers
    1..646
      /organism="Gossypium hirsutum"
      /mol_type="mRNA"
      /cultivar="Acala Maxxa"
      /db_xref="taxon:3635"
      /tissue_type="immature fiber"
      /dev_stage="Six days post anthesis"
      /lab_host="XlII-Blue"
      /clone_lib="Six-day Cotton fiber"
      /note="Vector: pBluescript II KS+"
FEATURES
  source
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      Pred. No.:      9,67e-16      Length:      646
      Score:          246.00      Matches:      77
      Percent Similarity: 50.48%      Conservative: 29
      Best Local Similarity: 36.67%      Mismatches:  68
      Query Match:    23.54%      Indels:      36
      DB:             1           Gaps:        10
    US-09-980-758A-8 (1-209) x AI728644 (1-646)
    Qy  15 GluArgLysArgGluLeuAlaGlu---GluAlaSerThrSerPheSerProLeuLys 33
    Db  60 AAACGAAGTCAGAGCAGCTGAATGGAAGCTTCAGACAGAGCTTCTCATATCAAG 119
    Qy  34 LysThrLys-----LeuAsnAspSerSerAspSerSerProAsp--- 46
    Db  120 AGAAGAAAACACTGTTGGTTCTCGAGAAATTGCAAGATTAGAGTTAACTTACCAGCAT 179
    Qy  47 -----SerHisaspValIleValPheAlaValSer 56
    Db  180 GAGCTCGGAACCACTCGCATCTTTTCGAAATTCGTCGACAAAGCCTATTATTAGCTACT 239
    Qy  57 SerSerSerValAlaSerSerAlaAlaLeuAlaSerAspGluCysSerValThrIleGly 76
    Db  240 TCCTCG-----GGTCTTGTGGAGTGCTTTCCGAGATATGTTTCGGTCTCTTCTCC 293
    Qy  77 GlyGluGluSerAspGlnSerSerIleSerSerGlyCysPheThrSerGluSerLys 96
    Db  294 GGCAATTCATCG-----GCTTCTCGTTTTCGAGCAACGAGTCGTGT 335
    Qy  97 GluIleAlaLysAsnSerSerPheGlyValAspLeuGluAspHisGlnIleGluThr 116
    Db  336 GATATTCTCAAGATAGCTTGAGATTC---GTAGATCTAGAGCGGACGAGTTTGTAAACT 392
```


JOURNAL
COMMENT

Unpublished (2004)
Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
UBC Biotechnology Laboratory, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 1Z3
Tel: 1-604-822-0282
Fax: 1-604-822-6097
Email: bohlmann@interchange.ubc.ca
Plate: WS02516 row: J column: 17
High quality sequence stop: 919
POLYA=Yes.

FEATURES

source

Location/Qualifiers

1..919

/organism="Populus balsamifera subsp. trichocarpa"

/mol_type="mrna"

/cultivar="Wild clone"

/sub_species="trichocarpa"

/db_xref="taxon:3694"

/clone="WS02516_J17"

/sex="Male"

/lab_host="E. coli DH10B T1 phage resistant cells"

/clone_lib="PT-MB-N-A-15"

/note="Vector: pBluescript II SK (+) XR; Site 1: EcoRI (5' end of cDNA); Site 2: XhoI (3' end of cDNA); Terminal vegetative buds from 20 year old trees harvested near Corvallis, Oregon on September 19th, 2001. cDNA was prepared from 5 micrograms of mRNA and directionally ligated into the pBluescript II SK (+) XR vector using the pBluescript II XR cDNA Library Construction Kit according to manufacturer's instructions with modifications (Stratagene). Plasmid DNA was then transformed by electroporation into DH10B cells (Invitrogen) for propagation. Normalization was applied according to published methods (Bonaldo M.F. et al. (1996) Genome Research 6(9):791) in order to reduce the abundance of highly expressed transcripts."

ORIGIN

Alignment Scores:

Pred. No.:	8,698-15	Length:	919
Score:	239.00	Matches:	76
Percent Similarity:	55.87%	Conservative:	43
Best Local Similarity:	35.68%	Mismatches:	65
Query Match:	22.87%	Indels:	29
DB:	7	Gaps:	12

US-09-980-758A-8 (1-209) x CV242992 (1-919)

Qy 6 LysAanProArgGluLys-LysMetSerGluArgLysArgGluLeuAlaGlu----- 22
 Db 913 AAGAATGGAGAGCGCGGAGGATAGTAAGCA-----ATAGCTGAACCTGGAAAT 863
 Qy 23 ----GluAlaSerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSe 41
 Db 862 TCTAGAACTTCAGTCACAGATTCTCT-----AAGAAATGAATTTGATTTTGACGA 809
 Qy 41 rAspSerSerPro-----AspSerHisAspValIleValPheAlaVa 55
 Db 808 GTTATAGCTTACCTCGTTTAATTTCAAGCTCCAAGCTCAT-----CTTGCACCACTAT 755
 Qy 55 lSerSerSerValAlaSerSerAlaAlaLeuAlaSerAspGluCysSerValThrI 75
 Db 754 GTCCACCGACAAATTTGATTCTCGCGGCTTCATCGAAATCTGATCGCTTATTAACC-- 697
 Qy 75 edgLyGluGluAspAspGlnSerSerSerIleSerSerGlyCysPheThrSerGlus 95
 Db 696 ----GGCAATTCAGCTGTGGCGACTCTCCGGTTTCCTGC---TGCTCCAGCAATGAATC 644
 Qy 95 rlyGluLeuAlaLysAsnSerSerPheGlyValAspLeuGluAspHisGlnIleGl 115
 Db 643 GATCAAGGTTGTGAAGGACAGCTTGAGGTTT---ATAGATCTGGAGCGCAAG-----AG 593

Qy 115 uThrGluThrGluThrSerThrPheIleThrSerAsnPheArgLysGluThrSerProVa 135
 Db 592 TTCGAAACGAAAGCTCGACGTCGAATTCAGAGAAATTCAGTAGAGACACCACTCTTC 533
 Qy 135 lSerGlu-----GlyLeuGlyGluThrThrGluMetGluSerSerAlaThrLy 153
 Db 532 AAGCGATTTTCACGGGATGACTCGCGGAGCGCTGGAGAAAGAAAGAAATTCACAG 473
 Qy 153 sAtqLysGlnProGlyValArgLysThrProThrAlaAlaGluIleGluAspLeuPheSe 173
 Db 472 GAGAAAGTCACCGCTGTG---AAATGCCGAGTCAGGCTGAGATCGATCGTTTTCGC 416
 Qy 173 rGluLeuGluSerProAspAspLysLysGlnPheIleGluLysThrAsnPheAspIl 193
 Db 415 GGGGGCAGAGAGA-----GAGGAGCAGAAAGATTTGCAGAGAAAGTACAACTACGATGT 362
 Qy 193 eValAsnAspGluProLeuGluGlyArgTyLysTip 205
 Db 361 TGTGAAGGATTTGCCAGTGGAGGGTGCCTACCACTGG 325

RESULT 14

CF212120

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..888

/organism="Vitis vinifera"

/mol_type="mrna"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clones="CAST0004_IIF_A05"

/sex="Hermaphrodite"

/dev_stage="Pre-bloom (10-11 days before bloom)"

/lab_host="DHSalpha"

/clone_lib="Vitis vinifera cv. cabernet sauvignon Stem -"

CAST"

/note="Organ: Stem; Vector: pNDR; Site 1: sfiI; Site 2: sfiI; CAST is a cDNA library of Vitis vinifera cv. 'Cabernet Sauvignon' stems. Samples were collected May 13, 2002 from pre-bloom plants (10-11 days before bloom), pre-veraison. Sampled vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows: 5'-AAGCAGTGTATCAACAGATGCGCATACGCGCGG-3' and 5'-ATTCTAGGCGCGCGCGCATG-dt(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

ORIGIN

	:::	230	TGTTCA---AGTCCTGGCTTGAAGAATTATCTGATCATGATCGTGTTTCGACTTCATGTTCG	286
Dd				
	:::	91	PheThrSerGluSerLysGluIleAlaLysAsnSerSerPheGlyValAspLeuGlu	110
Qy				
	:::	287	TCCAGTCCACAGTCAGTGAGAGATAGAA-----TTTGTAGATCTGAAG	331
Dd				
	:::	111	AspHisGlnIleGluThrGluThrGluThrSerThrPhe-	123
Qy				
	:::	332	GATGAGAGTGTGATGTGGAGCTGAACATCGACGTATTATGGATGCAGAAAAGGACA	391
Dd				
	:::	124	-----IleThrSerAsnPheArgLysGluThrSerProValSerGluGlyLeuGly	140
Qy				
	:::	392	GACGCGACGCTGTCCAGCGAGCTTGAACCTGAAGCTGGAGAAGAATCAGACGCCCTG---	448
Dd				
	:::	141	GluThrThrThrGluMetGluSerSerSerAlaThrLysArgLysGlnProGlyValArg	160
Qy				
	:::	449	---GATTCACTGCGAAGCCATCATCAGAGGCAAACTCTGCCCGTAGATCAACGGTGGAG	505
Dd				
	:::	161	LysThrProThraAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAsp	180
Qy				
	:::	506	AGCATGCTCGCAAGTCTGAATTTGAGGACTTCTTCGCTGAAGCTGAG-----	553
Dd				
	:::	181	LysLys-----LysGlnPhelIleGlyLysTyAsnPheAspIleValAsnAspGluPro	198
Qy				
	:::	554	AAAAAGCTCGTAACAATTTCTCAGAAGTATAACTTCGACTTCGTGTAAGAGGAGGCCA	613
Dd				
	:::	199	LeuGluGlyArgTyrLysTrp	205
Qy				
	:::	614	ATGGAAGGACCGTTACAAGTG	634
Dd				

Search completed: September 30, 2005, 13:54:39
Job time : 3174 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 30, 2005, 09:14:02 ; Search time 81 Seconds
(without alignments)
997.937 Million cell updates/sec

Title: US-09-980-758A-8
Perfect score: 1045
Sequence: 1 PDDLKPNREKMSERKREL.....NFDIVNDEPLEGRYKWDRLX 209

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1044	99.9	208	4 AAB47001	Aab47001 Plant D-1
2	1007	96.4	212	3 AAY44337	Aay44337 Arabidops
3	1007	96.4	212	5 AAE25103	Aae25103 Arabidops
4	969	92.7	196	5 AAE25104	Aae25104 Arabidops
5	351.5	33.6	207	3 AAY44338	Aay44338 Arabidops
6	351.5	33.6	207	5 AAE25105	Aae25105 Arabidops
7	346.5	33.2	195	5 AAE25106	Aae25106 Arabidops
8	184	17.6	206	4 AAB47004	Aab47004 Plant D-1
9	177	16.9	209	2 AAW98179	Aaw98179 Arabidops
10	177	16.9	209	3 AAG17611	Aag17611 Arabidops
11	177	16.9	209	3 AAG38486	Aag38486 Arabidops
12	177	16.9	209	5 AAE25110	Aae25110 Arabidops
13	177	16.9	209	8 ADN72203	Adn72203 Thale cre
14	175.5	16.8	191	3 AAY44335	Aay44335 Arabidops
15	175.5	16.8	191	3 AAG15426	Aag15426 Arabidops
16	175.5	16.8	191	3 AAG42858	Aag42858 Arabidops
17	175.5	16.8	191	5 AAE25101	Aae25101 Arabidops
18	174	16.7	171	3 AAG42859	Aag42859 Arabidops
19	174	16.7	171	3 AAG15427	Aag15427 Arabidops
20	172	16.5	205	3 AAP01952	Aap01952 Cyclin de
21	172	16.5	205	3 AAB27254	Aab27254 Soybean c
22	168.5	16.1	196	3 AAB27259	Aab27259 Chenopodi
23	168.5	16.1	196	3 AAY44340	Aay44340 Chenopodi
24	168.5	16.1	196	5 AAE25108	Aae25108 Chenopodi
25	162.5	15.6	256	3 AAG40486	Aag40486 Arabidops

26	162.5	15.6	289	3 AAB27262	Aab27262 Arabidops
27	162.5	15.6	289	3 AAG40485	Aag40485 Arabidops
28	162.5	15.6	289	5 AAE25109	Aae25109 Arabidops
29	162.5	15.6	289	5 AAU72581	Aau72581 Arabidops
30	162.5	15.6	289	8 ADN72347	Adn72347 Thale cre
31	159	15.2	176	3 AAY44336	Aay44336 Arabidops
32	159	15.2	176	5 AAE25102	Aae25102 Arabidops
33	159	15.2	183	3 AAG38487	Aag38487 Arabidops
34	159	15.2	183	3 AAG17612	Aag17612 Arabidops
35	155	14.8	222	5 AAE25111	Aae25111 Arabidops
36	154.5	14.8	201	3 AAG40487	Aag40487 Arabidops
37	153	14.6	262	5 ABG65670	Abg65670 OsrICK 2 p
38	152	14.5	216	2 AAW98180	Aaw98180 Arabidops
39	152	14.5	222	8 ADN72351	Adn72351 Thale cre
40	150.5	14.4	137	5 AAE25107	Aae25107 Arabidops
41	149	14.3	194	5 ABG65691	Abg65691 Rice OsrIC
42	147.5	14.1	190	3 AAB27258	Aab27258 Wheat cyc
43	144.5	13.8	136	3 AAY44339	Aay44339 Arabidops
44	139	13.3	419	8 ADR86387	Adr86387 Aspergill
45	139	13.3	446	8 ADR86528	Adr86528 Aspergill

ALIGNMENTS

RESULT 1

AAB47001
ID AAB47001 standard; protein; 208 AA.

XX AAB47001;

AC AAB47001;

XX 22-MAR-2001 (first entry)

XX Plant D-like cyclin inhibitor BRO4.

XX Plant; D-like cyclin inhibitor gene; BRO4; hyperplastic; variant;

XX growth rate; dividing cells; inactivation; protoplast; seed; root cell;

XX meristem; leaf.

XX Arabidopsis thaliana.

XX Key Location/Qualifiers

XX Protein 13..208

XX FT /label= BRO4

XX WQ200069883-A1.

XX 23-NOV-2000.

XX 15-MAY-2000; 2000WO-US013379.

XX 14-MAY-1999; 99US-0134373P.

XX (HUTC-) HUTCHINSON CANCER RES CENT FRED.

XX Roberts J, Kelly B;

XX WPI; 2001-024998/03.

XX N-PSDB; AAC85201.

XX Functionally inactivating expression of plant D-like cyclin inhibitor

XX gene for producing a hyperplastic variant plant, modulating the growth

XX and/or yield of plants, and increasing the proportion of dividing cells.

XX Claim 15; Page 41-42; 50pp; English.

XX The sequence given in AAB47001 represents a plant D-like cyclin

XX inhibitor, BRO4. The DNA encoding this sequence may be used to produce a

XX hyperplastic variant plant, increase the growth rate of a plant, or

XX increase the proportion of dividing cells in a plant cell population,

XX relative to a wild-type plant, by functionally inactivating the

XX expression of a plant D-like cyclin inhibitor gene in a plant. The DNA

XX sequence is homologous to a sequence present in a D-like cyclin inhibitor

CC gene and when integrated at the corresponding locus, functionally
 CC inactivates plant D-like cyclin inhibitor protein expression. BR04 is
 CC useful for producing hyperplastic variant plants, increasing the growth
 CC rate of a plant and for increasing the proportion of dividing cells in a
 CC plant cell population comprising protoplast, seeds, root cells, meristem
 CC cells or leaf cells
 XX
 SQ Sequence 208 AA;

Query Match 99.9%; Score 1044; DB 4; Length 208;
 Best Local Similarity 100.0%; Pred. No. 2.9e-81;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRDLPKNPREKMSRKRELAEEASTSFSPKTKTKLNDSSDSSPDSDHVDIVFAVSSSV 60
 DB 1 PRDLPKNPREKMSRKRELAEEASTSFSPKTKTKLNDSSDSSPDSDHVDIVFAVSSSV 60

QY 61 ASSAALASDECSTVTGGESDQSSISGCGFTSESKEIAKNSSSGVDLEDHQIETETET 120
 DB 61 ASSAALASDECSTVTGGESDQSSISGCGFTSESKEIAKNSSSGVDLEDHQIETETET 120

QY 121 STFITSNFRKETSPPVSEGLGETTTEMESSATKRGKOPGVRKPTPTAAEIEDLFSELESPPD 180
 DB 121 STFITSNFRKETSPPVSEGLGETTTEMESSATKRGKOPGVRKPTPTAAEIEDLFSELESPPD 180

QY 181 KKKQFIEKYNFDIVNDEPLEGKYKWDRL 208
 DB 181 KKKQFIEKYNFDIVNDEPLEGKYKWDRL 208

RESULT 2
 AAY44337
 ID AAY44337 standard; protein; 212 AA.

XX AC AAY44337;
 XX DT 29-FEB-2000 (first entry)
 XX DE Arabidopsis thaliana CDK inhibitor, ICN2.
 XX KW Cyclin-Dependent Kinase inhibitor; CDK; Interactor of Cyclin 2; ICN2;
 KW Cdc2a; D-class cyclin; Cycl1; Cycl2; Cycd3; morphogenesis;
 KW antisense construct; tissue-specific promoter; transgenic plant;
 KW male sterility.
 XX OS Unidentified.
 XX PN WO9964599-A1.
 XX PD 16-DEC-1999.
 XX PF 08-JUN-1999; 99WO-CA000532.
 XX PR 08-JUN-1998; 98CA-02235978.
 XX PR 31-DEC-1998; 98CA-02256121.
 XX PA (MIAC) AGRIC & AGRI-FOOD CANADA.
 XX PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
 XX PA (CAN) NAT RES COUNCIL CANADA.
 XX PI Wang H, Fowke LC, Crosby WL;
 XX WPI; 2000-097540/08.
 XX DR N-PSDB; AA229417.
 XX PT Modifying plant cell development using nucleic acid encoding inhibitor of
 PT cyclin-dependent kinase, or corresponding antisense sequence, e.g. for
 PT inducing male sterility.
 XX PS Disclosure; Fig 7; 58pp; English.
 XX CC The present protein sequence is ICN2, which inhibits A. thaliana Cyclin-
 CC Dependent Kinase (CDK). Interactor of Cyclin 2 (ICN2) interacts with

CC Cdc2a, D-class cyclins, CycD1, CycD2 and CycD3 and shares functional and
 CC sequence similarity with ICK1. Growth, morphogenesis, multiplication,
 CC enlargement, differentiation and maturation of plant cells can be
 CC modified by transforming them with nucleic acid encoding CDK inhibitor or
 CC antisense construct complementary to the inhibitor gene, operably linked
 CC to a tissue-specific promoter. The transgenic plants exhibit alteration
 CC of traits such as petals, male sterility and ability to set seeds
 XX
 SQ Sequence 212 AA;

Query Match 96.4%; Score 1007; DB 3; Length 212;
 Best Local Similarity 99.5%; Pred. No. 4.4e-78;
 Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 KNPPEKMSRKRELAEEASTSFSPKTKTKLNDSSDSSPDSDHVDIVFAVSSSVASAA 65
 DB 10 KNPPEKMSRKRELAEEASTSFSPKTKTKLNDSSDSSPDSDHVDIVFAVSSSVASAA 69

QY 66 LASDECSTVTGGESDQSSISGCGFTSESKEIAKNSSSGVDLEDHQIETETETET 125
 DB 70 LASDECSTVTGGESDQSSISGCGFTSESKEIAKNSSSGVDLEDHQIETETETET 129

QY 126 SNFRKETSPPVSEGLGETTTEMESSATKRGKOPGVRKPTPTAAEIEDLFSELESPPD 185
 DB 130 SNFRKETSPPVSEGLGETTTEMESSATKRGKOPGVRKPTPTAAEIEDLFSELESPPD 189

QY 186 IEKYNFDIVNDEPLEGKYKWDRL 208
 DB 190 IEKYNFDIVNDEPLEGKYKWDRL 212

RESULT 3
 AAE25103
 ID AAE25103 standard; protein; 212 AA.

XX AC AAE25103;
 XX DT 30-OCT-2002 (first entry)
 XX DE Arabidopsis thaliana ICN2 protein #1.
 XX KW Plant development; cyclin-dependent kinase; CDK inhibitor; ICK1; ICK2;
 KW ICN2; ICN; ICN7; ICN8; ICN9; morphogenesis; maturation; enlargement;
 KW plant breeding; growth.
 XX OS Arabidopsis thaliana.
 XX PN WO200250292-A2.
 XX PD 27-JUN-2002.
 XX PF 18-DEC-2001; 2001WO-CA001825.
 XX PR 18-DEC-2000; 2000US-0255908P.
 XX PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
 XX PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
 XX PI Wang H, Zhou Y, Fowke LC;
 XX WPI; 2002-519888/55.
 XX DR N-PSDB; AAD40765.
 XX PT Modifying plant development, e.g. growth or maturation, which is
 PT particularly useful in plant breeding, by introducing nucleic acids
 PT coding for cyclin-dependent kinase (CDK) inhibitor, cyclin or proteins
 PT that bind to CDK inhibitors.
 XX PS Disclosure; Fig 8A; 89pp; English.
 XX CC The invention relates to a method for the development of a plant. The
 CC method involves introducing into a plant cell a nucleic acid encoding a
 CC protein that binds or interacts with a cyclin-dependent kinase (CDK)

CC inhibitor polypeptide (such as ICK1, ICK2, ICN2, ICN6, ICN7, ICN8 and
CC ICDK), a cyclin polypeptide, a CDK, or a polypeptide that modulates the
CC degradation of a CDK inhibitor polypeptide. The method is useful for
CC modifying the growth and development of plants e.g. morphogenesis,
CC growth, multiplication, enlargement, differentiation or maturation of a
CC cell or plant. It is particularly useful in plant breeding. The present
CC sequence is A. thaliana ICN2 protein
XX
SQ Sequence 212 AA;

Query Match 96.4%; Score 1007; DB 5; Length 212;
Best Local Similarity 99.5%; Pred. No. 4.4e-78;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 KNPREKMSRKELAEASSTFSPLKTKLNDSSDSDSHDVIVFAVSSSVASSAA 65
DB 10 KNPREKMSRKELAEASSTFSPLKTKLNDSSDSDSHDVIVFAVSSSVASSAA 69
QY 66 LASDECSVTIGGESDQSSISGGCFTSESKEIAKNSSFGVDLEDHQIETETSTFIT 125
DB 70 LASDECSVTIGGESDQSSISGGCFTSESKEIAKNSSFGVDLEDHQIETETSTFIT 129
QY 126 SNFRKETSPVSEGLGTTTTEMESSTATKRKQPGVRKPTPTAAEIEDLFSELESDDKKQKF 185
DB 130 SNFRKETSPVSEGLGTTTTEMESSTATKRKQPGVRKPTPTAAEIEDLFSELESDDKKQKF 189
QY 186 IEKYNFDVNDPELEGRYKWDRL 208
DB 190 IEKYNFDVNDPELEGRYKWDRL 212

RESULT 4
AAE25104
ID AAE25104 standard; protein; 196 AA.
XX
AC AAE25104;
DT 30-OCT-2002 (first entry)
XX
DE Arabidopsis thaliana ICN2 protein #2.
XX
KW Plant development; cyclin-dependent kinase; CDK inhibitor; ICK1; ICK2;
KW ICN2; ICN6; ICN7; ICN8; ICDK; morphogenesis; maturation; enlargement;
KW plant breeding; growth.
XX
OS Arabidopsis thaliana.
XX
PN WO200250292-A2.
XX
PD 27-JUN-2002.
XX
PF 18-DEC-2001; 2001WO-CA001825.
XX
PR 18-DEC-2000; 2000US-0255908P.
XX
PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
XX
PI Wang H, Zhou Y, Fowke LC;
XX
DR WPI; 2002-519888/55.
DR N-PSDB; AAD40765.
XX
PT Modifying plant development, e.g. growth or maturation, which is
PT particularly useful in plant breeding, by introducing nucleic acids
PT coding for cyclin-dependent kinase (CDK) inhibitor, cyclin or proteins
PT that bind to CDK inhibitors.
XX
PS Disclosure; Fig 8B; 89pp; English.
XX
CC The invention relates to a method for the development of a plant. The
CC method involves introducing into a plant cell a nucleic acid encoding a
CC protein that binds or interacts with a cyclin-dependent kinase (CDK)

CC inhibitor polypeptide (such as ICK1, ICK2, ICN2, ICN6, ICN7, ICN8 and
CC ICDK), a cyclin polypeptide, a CDK, or a polypeptide that modulates the
CC degradation of a CDK inhibitor polypeptide. The method is useful for
CC modifying the growth and development of plants e.g. morphogenesis,
CC growth, multiplication, enlargement, differentiation or maturation of a
CC cell or plant. It is particularly useful in plant breeding. The present
CC sequence is A. thaliana ICN2 protein
XX
SQ Sequence 196 AA;

Query Match 92.7%; Score 969; DB 5; Length 196;
Best Local Similarity 99.5%; Pred. No. 7.1e-75;
Matches 195; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 MSERKRELAEASSTFSPLKTKLNDSSDSDSHDVIVFAVSSSVASSAALASDECS 72
DB 1 MSERKRELAEASSTFSPLKTKLNDSSDSDSHDVIVFAVSSSVASSAALASDECS 60
QY 73 VTIGGESDQSSISGGCFTSESKEIAKNSSFGVDLEDHQIETETSTFITSNFRKET 132
DB 61 VTIGGESDQSSISGGCFTSESKEIAKNSSFGVDLEDHQIETETSTFITSNFRKET 120
QY 133 SPVSEGLGTTTTEMESSTATKRKQPGVRKPTPTAAEIEDLFSELESDDKKQFIEKYNFD 192
DB 121 SPVSEGLGTTTTEMESSTATKRKQPGVRKPTPTAAEIEDLFSELESDDKKQFIEKYNFD 180
QY 193 IVNDEPLEGRYKWDRL 208
DB 181 IVNDEPLEGRYKWDRL 196

RESULT 5
AAY44338
ID AAY44338 standard; protein; 207 AA.
XX
AC AAY44338;
DT 29-FEB-2000 (first entry)
XX
DE Arabidopsis thaliana CDK inhibitor, ICN6.
XX
KW Cyclin-Dependent Kinase inhibitor; CDK; Interactor of Cyclin 6; ICN6;
KW Cdc2a; D-Class cyclin; CycD1; CycD2; CycD3; morphogenesis;
KW antisense construct; tissue-specific promoter; transgenic plant;
KW male sterility.
XX
OS Unidentified.
XX
PN WO9964599-A1.
XX
PD 16-DEC-1999.
XX
PF 08-JUN-1999; 99WO-CA000532.
XX
PR 08-JUN-1998; 98CA-02235978.
PR 31-DEC-1998; 98CA-022356121.
XX
PA (MIAC) AGRIC & AGRI-FOOD CANADA.
PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
PA (CAN) NAT RES COUNCIL CANADA.
XX
PI Wang H, Fowke LC, Crosby WL;
XX
DR WPI; 2000-097540/08.
DR N-PSDB; AA229418.
XX
PT Modifying plant cell development using nucleic acid encoding inhibitor of
PT cyclin-dependent kinase, or corresponding antisense sequence, e.g. for
PT inducing male sterility.
XX
PS Disclosure; Fig 7; 58pp; English.
XX
CC The present protein sequence is ICN6, which inhibits A. thaliana Cyclin-

CC Dependent Kinase (CDK). Interactor of Cyclin 6 (ICN6) interacts with
CC Cdc2a, D-class cyclins, CycD1, CycD2 and CycD3 and shares functional
CC sequence similarity with ICN1. Growth, morphogenesis, multiplication,
CC enlargement, differentiation and maturation of plant cells can be
CC modified by transforming them with nucleic acid encoding CDK inhibitor or
CC antisense construct complementary to the inhibitor gene, operably linked
CC to a tissue-specific promoter. The transgenic plants exhibit alteration
CC of traits such as petals, male sterility and ability to set seeds
XX
XX
SQ Sequence 207 AA;

Query Match 33.6%; Score 351.5; DB 3; Length 207;
Best Local Similarity 44.5%; Pred. No. 6.3e-22;
Matches 93; Conservative 30; Mismatches 57; Indels 29; Gaps 10;
QY 9 REKMSERKRLAEASSTSFSLKTKLNDSDD--SSPDSDHVDVFAVSSSSVASSAAL 66
DB 11 REMSETPKRSEYEGSN-----IKRWRLDDDDVLRSPTR-----TLSSSSSSSLAYS 59
QY 67 ASDE---CSVTIGGESDQ-SSSISGCGFTSESKEIAKNSSSFGVDLEDHQIETETST 122
DB 60 VSDSGGFCVALSEEDDHLSSISGCGSSSETNEIATRLPF--SDLEAHEI-SETEIST 116
QY 123 FITSNFRKETSVPSEGLGET-----TTEMSSSATKPKQGVKRTPTAAELDLFSELE 176
DB 117 LLTNFRKQGISSENELGETAEMDSATTEMRDQRKTEKKK-MEKSPTQAEILDFFSAE 175
QY 177 SPDDKKKQFIEKNFDIVNDEPLEGRYKW 205
DB 176 RYE--QKRFTKYNIDVNDTPLEGRYQW 202

RESULT 6
AAE25105
ID AAE25105 standard; protein; 207 AA.
XX
AC AAE25105;
XX
DT 30-OCT-2002 (first entry)
XX
DE Arabidopsis thaliana ICN6 protein #1.
XX
KW Plant development; cyclin-dependent kinase; CDK inhibitor; ICN1; ICN2;
KW ICN2; ICN6; ICN7; ICN8; ICNK; morphogenesis; maturation; enlargement;
KW plant breeding; growth.
XX
OS Arabidopsis thaliana.
XX
FN WO200250292-A2.
XX
PD 27-JUN-2002.
XX
PF 18-DEC-2001; 2001WO-CA001825.
XX
PR 18-DEC-2000; 2000US-0255908P.
XX
PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
XX
PI Wang H, Zhou Y, Fowke LC;
XX
WPI; 2002-519888/55.
DR N-PSDB; AAD40766.
XX
PT Modifying plant development, e.g. growth or maturation, which is
PT particularly useful in plant breeding, by introducing nucleic acids
PT coding for cyclin-dependent kinase (CDK) inhibitor, cyclin or proteins
PT that bind to CDK inhibitors.
XX
PS Disclosure; Fig 9A; 89pp; English.
XX
XX The invention relates to a method for the development of a plant. The
CC method involves introducing into a plant cell a nucleic acid encoding a

CC protein that binds or interacts with a cyclin-dependent kinase (CDK)
CC inhibitor polypeptide (such as ICN1, ICN2, ICN6, ICN7, ICN8 and
CC ICNK), a cyclin polypeptide, a CDK, or a polypeptide that modulates the
CC degradation of a CDK inhibitor polypeptide. The method is useful for
CC modifying the growth and development of plants e.g. morphogenesis,
CC growth, multiplication, enlargement, differentiation or maturation of a
CC cell or plant. It is particularly useful in plant breeding. The present
CC sequence is A. thaliana ICN6 protein
XX
XX
SQ Sequence 207 AA;

Query Match 33.6%; Score 351.5; DB 5; Length 207;
Best Local Similarity 44.5%; Pred. No. 6.3e-22;
Matches 93; Conservative 30; Mismatches 57; Indels 29; Gaps 10;
QY 9 REKMSERKRLAEASSTSFSLKTKLNDSDD--SSPDSDHVDVFAVSSSSVASSAAL 66
DB 11 REMSETPKRSEYEGSN-----IKRWRLDDDDVLRSPTR-----TLSSSSSSSLAYS 59
QY 67 ASDE---CSVTIGGESDQ-SSSISGCGFTSESKEIAKNSSSFGVDLEDHQIETETST 122
DB 60 VSDSGGFCVALSEEDDHLSSISGCGSSSETNEIATRLPF--SDLEAHEI-SETEIST 116
QY 123 FITSNFRKETSVPSEGLGET-----TTEMSSSATKPKQGVKRTPTAAELDLFSELE 176
DB 117 LLTNFRKQGISSENELGETAEMDSATTEMRDQRKTEKKK-MEKSPTQAEILDFFSAE 175
QY 177 SPDDKKKQFIEKNFDIVNDEPLEGRYKW 205
DB 176 RYE--QKRFTKYNIDVNDTPLEGRYQW 202

RESULT 7
AAE25106
ID AAE25106 standard; protein; 195 AA.
XX
AC AAE25106;
XX
DT 30-OCT-2002 (first entry)
XX
DE Arabidopsis thaliana ICN6 protein #2.
XX
KW Plant development; cyclin-dependent kinase; CDK inhibitor; ICN1; ICN2;
KW ICN2; ICN6; ICN7; ICN8; ICNK; morphogenesis; maturation; enlargement;
KW plant breeding; growth.
XX
OS Arabidopsis thaliana.
XX
FN WO200250292-A2.
XX
PD 27-JUN-2002.
XX
PF 18-DEC-2001; 2001WO-CA001825.
XX
PR 18-DEC-2000; 2000US-0255908P.
XX
PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
XX
PI Wang H, Zhou Y, Fowke LC;
XX
WPI; 2002-519888/55.
DR N-PSDB; AAD40766.
XX
PT Modifying plant development, e.g. growth or maturation, which is
PT particularly useful in plant breeding, by introducing nucleic acids
PT coding for cyclin-dependent kinase (CDK) inhibitor, cyclin or proteins
PT that bind to CDK inhibitors.
XX
PS Disclosure; Fig 9B; 89pp; English.
XX
XX The invention relates to a method for the development of a plant. The
CC method involves introducing into a plant cell a nucleic acid encoding a

CC protein that binds or interacts with a cyclin-dependent kinase (CDK)
CC inhibitor polypeptide (such as ICK1, ICK2, ICN6, ICN7, ICN8 and
CC ICK9), a cyclin polypeptide, a CDK, or a polypeptide that modulates the
CC degradation of a CDK inhibitor polypeptide. The method is useful for
CC modifying the growth and development of plants e.g. morphogenesis,
CC growth, multiplication, enlargement, differentiation or maturation of a
CC cell or plant. It is particularly useful in plant breeding. The present
CC sequence is A. thaliana ICN6 protein
XX
SQ Sequence 195 AA;
Query Match 33.2%; Score 346.5; DB 5; Length 195;
Best Local Similarity 45.4%; Pred. No. 1.6e-21;
Matches 93; Conservative 27; Mismatches 58; Indels 27; Gaps 10;
QY 13 MSERKRELAEEASTSFSPKTKLNDSSD--SSPDSDHIVFAVSSSVASSAALASDE 70
DB 1 MSETKPKRDEYEG---SNIKRMRLDDDDVLRSPTR-----TLSSSSSSSLAYSVDS 51
QY 71 ---CSVTIGGEESDQ-SSSISGCTTSSEKEIAKNSSSFGVDLHQIETETSTFTS 126
DB 52 GGFCSVALSEEDDHLSSISGSSSTWEIATRLPF--SDLEAHEI-SETEISTLTN 108
QY 127 NFRKETSPPVSEGLGET-----TTEMSSSATKQKQGVKTKPTAAEIDLSELESPPD 180
DB 109 NFRKQGISSENIGETAEMDSATTEMQRKTEKKK-MEKSPTQAELODFFSAERYE- 166
QY 181 KKQFIEKYNFDVNDPELEGRYKW 205
DB 167 -QKRFTEKYNVDVNDTPLEGRYQW 190
RESULT 8
AAB47004
ID AAB47004 standard; protein; 206 AA.
XX
AC AAB47004;
XX
XX
XX 22-MAR-2001 (first entry)
XX Plant D-like cyclin inhibitor BRO3.
XX
XX Plant; D-like cyclin inhibitor gene; BRO4; hyperplastic; variant;
XX growth rate; dividing cells; inactivation; protoplast; seed; root cell;
XX meristem; leaf.
XX
XX Arabidopsis thaliana.
XX
XX Key Location/Qualifiers
XX Protein 20..202
XX /label= BRO3
XX
XX WO200069883-A1.
XX
XX 23-NOV-2000.
XX
XX 15-MAY-2000; 2000WO-US013379.
XX
XX 14-MAY-1999; 99US-0134373P.
XX
XX (HUTC-) HUTCHINSON CANCER RES CENT FRED.
XX
XX Roberts J, Kelly B;
XX
XX WPI; 2001-024998/03.
XX N-PSDB; AAC85204.
XX
XX Functionally inactivating expression of plant D-like cyclin inhibitor
XX gene for producing a hyperplastic variant plant, modulating the growth
XX and/or yield of plants, and increasing the proportion of dividing cells.
XX
XX Example 1; Page 40-41; 50pp; English.
XX

CC The sequence given in AAB47004 represents a plant D1 cyclin inhibitor,
CC BRO3. The DNA encoding this sequence was isolated using a yeast two
CC hybrid screen. The BRO3 protein was found to contain a seven amino acid
CC sequence cyclin binding domain similar to that of BRO1, BRO2 and BRO4
CC (see also AAB47005-6). The DNA encoding this sequence is homologous to a
CC sequence present in a D-like cyclin inhibitor gene and when integrated at
CC the corresponding locus, functionally inactivates plant D-like cyclin
CC inhibitor protein expression. The BRO4 coding sequence may be used to
CC produce a hyperplastic variant plant, increase the growth rate of a
CC plant, or increase the proportion of dividing cells in a plant cell
CC population, relative to a wild-type plant, by functionally inactivating
CC the expression of a plant D-like cyclin inhibitor gene in a plant. BRO4
CC is useful for increasing the proportion of dividing cells in a plant cell
CC population comprising protoplast, seeds, root cells, meristem cells or
CC leaf cells
XX
SQ Sequence 206 AA;
Query Match 17.6%; Score 184; DB 4; Length 206;
Best Local Similarity 30.4%; Pred. No. 1.4e-07;
Matches 69; Conservative 43; Mismatches 73; Indels 42; Gaps 14;
QY 1 PRDLPKNPKKMSERKRELAEEASTSFSPKTKLNDSSSDSPDSDHIVFAVSSSS- 59
DB 1 PRDLP-----RDVVEGVTT-TTKRRKMEEEVD-LVESRILSPCVQATNR 46
QY 60 ---VASSAALASDECSVTIGGEES-----DOSSSISGCTTSSEKEIAKNSSSPG 106
DB 47 GGIVARNASAGSETSVIVRRRDSPPVEQCQIEEDSSVSC-CSTSEK--SKRRIEF- 102
QY 107 VLEHDHQ-IETETSTFTSINFRKETSPPVSEGLGETTTEMSSSATKQKQGVKTKPTA 165
DB 103 VDLEENNGDDRETETS-WIYDNLK--SEESNMDSVAVEDVESRRRLKSLHETVKE 159
QY 166 AEIEDLSELESPPDDKKQFIE---KYNFDVNDPEL-BGRYKWDRL 208
DB 160 AELEDFQVAEK--DLRNKLLCSMKYNDFEKFDEPLGGRYEHWVKL 204
RESULT 9
AAW98179
ID AAW98179 standard; protein; 209 AA.
XX
AC AAW98179;
XX
XX 05-JUL-1999 (first entry)
XX
XX Arabidopsis cyclin-dependent kinase inhibitor FL39.
XX
XX Cyclin-dependent kinase inhibitor; CDK inhibitor; CKI; CDK1; FL39;
XX plant development; transgenic plant; cell cycle; growth regulator;
XX herbicide.
XX
XX Arabidopsis thaliana.
XX
XX Key Location/Qualifiers
XX Region 4..14
XX /note= "repeated motif"
XX Peptide 23..26
XX /note= "putative nuclear localisation signal"
XX Region 68..78
XX /note= "repeated motif"
XX Protein 75..209
XX /note= "this protein region is specifically claimed in
XX Claim 1(c)"
XX Region 79..98
XX /note= "PEST-rich region, characteristic of unstable
XX proteins"
XX
XX WO9914331-A2.
XX
XX 25-MAR-1999.
XX

PR	02-JUL-1999;	99US-0142055P.
PR	06-JUL-1999;	99US-0142390P.
PR	08-JUL-1999;	99US-0142803P.
PR	09-JUL-1999;	99US-0142927P.
PR	12-JUL-1999;	99US-0143277P.
PR	13-JUL-1999;	99US-0143342P.
PR	14-JUL-1999;	99US-0143624P.
PR	15-JUL-1999;	99US-0144005P.
PR	16-JUL-1999;	99US-0144085P.
PR	16-JUL-1999;	99US-0144086P.
PR	19-JUL-1999;	99US-0144325P.
PR	19-JUL-1999;	99US-0144331P.
PR	19-JUL-1999;	99US-0144332P.
PR	19-JUL-1999;	99US-0144333P.
PR	19-JUL-1999;	99US-0144334P.
PR	19-JUL-1999;	99US-0144335P.
PR	20-JUL-1999;	99US-0144352P.
PR	20-JUL-1999;	99US-0144632P.
PR	20-JUL-1999;	99US-0144884P.
PR	21-JUL-1999;	99US-0144814P.
PR	21-JUL-1999;	99US-0145086P.
PR	21-JUL-1999;	99US-0145088P.
PR	22-JUL-1999;	99US-0145085P.
PR	22-JUL-1999;	99US-0145087P.
PR	22-JUL-1999;	99US-0145089P.
PR	22-JUL-1999;	99US-0145192P.
PR	23-JUL-1999;	99US-0145145P.
PR	23-JUL-1999;	99US-0145218P.
PR	23-JUL-1999;	99US-0145224P.
PR	26-JUL-1999;	99US-0145276P.
PR	27-JUL-1999;	99US-0145913P.
PR	27-JUL-1999;	99US-0145918P.
PR	27-JUL-1999;	99US-0145919P.
PR	28-JUL-1999;	99US-0147302P.
PR	05-AUG-1999;	99US-0147192P.
PR	05-AUG-1999;	99US-0147260P.
PR	06-AUG-1999;	99US-0147303P.
PR	06-AUG-1999;	99US-0147416P.
PR	09-AUG-1999;	99US-0147493P.
PR	09-AUG-1999;	99US-0147935P.
PR	10-AUG-1999;	99US-0148171P.
PR	11-AUG-1999;	99US-0148319P.
PR	12-AUG-1999;	99US-0148341P.
PR	13-AUG-1999;	99US-0148565P.
PR	13-AUG-1999;	99US-0148684P.
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PR	18-AUG-1999;	99US-0149426P.
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PR	30-AUG-1999;	99US-0151303P.
PR	31-AUG-1999;	99US-0151438P.
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PR	13-SEP-1999;	99US-0153758P.
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PR	05-OCT-1999;	99US-015753P.
PR	06-OCT-1999;	99US-0157865P.
PR	07-OCT-1999;	99US-0158029P.
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PR	12-OCT-1999;	99US-0158369P.
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PR	18-OCT-1999;	99US-0159584P.
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Query Match 16.9%; Score 177; DB 3; Length 209;		
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Matches 65; Conservative 44; Mismatches 73; Indels 30; Gaps 13;		
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XX	AC AAG38486;	
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DT	18-OCT-2000 (first entry)	
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 47487.	
XX	Protein identification; signal transduction pathway; metabolic pathway;	
KW	hybridisation assay; genetic mapping; gene expression control; promoter;	

KW termination sequence.
XX Arabidopsis thaliana.
XX EP1033405-A2.
XX PD 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
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PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.

XX Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 98.
XX plant; transgenic; E2Fa/Dpa transcription factor; growth regulator;
KW animal feed product; thale cress; cell wall biosynthesis;
KW nitrogen metabolism; carbon metabolism.
XX Arabidopsis thaliana.
OS WO2004035798-A2.
XX 29-APR-2004.
XX 20-OCT-2003; 2003WO-EP011658.
XX 18-OCT-2002; 2002EP-00079408.
XX (CROP-) CROPDISEIGN NV.
XX Inze D, De Veylder L, Vlieghe K;
XX WPI: 2004-348466/32.
DR N-PSDB; ADN72202.
XX
XX Altering plant characteristics, useful for producing plants for enzyme or
PT pharmaceutical production comprises modifying in a plant, expression of
PT one or more nucleic acids and/or modifying level or activity of one or
PT more proteins.
XX Claim 1; SEQ ID NO 98; 134pp; English.
XX
XX This invention relates to a novel method for altering one or more plant
CC characteristics. Specifically, it refers to identifying genes that are up
CC - or down-regulated in transgenic plants overexpressing the heterodimeric
CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to
CC alter plant characteristics accordingly. The present invention describes
CC generating transgenic plants for the production of growth regulators,
CC enzymes, therapeutics, pharmaceuticals and animal feed products, where
CC the altered plant characteristics are selected from increased yield or
CC biomass, enhanced survival capacity, stress tolerance, plant architecture
CC or physiology, altered endoreplication, biochemistry, signal
CC transduction, storage lipid mobilisation and/or altered photosynthesis,
CC each relative to the corresponding wild type plants. Accordingly, these
CC sequences can also be useful as positive or negative selectable markers
CC during transformation of cells or tissues. The identified genes play a
CC role in a variety of biological processes such as DNA replication, cell
CC wall biosynthesis, nitrogen and/ or carbon metabolism or they function as
CC transcription factors. This polypeptide sequence is thale cress protein
CC expressed by a gene upregulated 1.3 fold or more in plants overexpressing
CC the E2Fa/Dpa transcription factor, given in an exemplification of the
XX invention.
XX
SQ Sequence 209 AA;
Query Match 16.9%; Score 177; DB 8; Length 209;
Best Local Similarity 30.7%; Pred. No. 5.7e-07;
Matches 65; Conservative 44; Mismatches 73; Indels 30; Gaps 13;
QY 16 KRLEAEASSTFSPLKTKLNDSDSPSHDIVFAVSSSS---VASSAALASDEC 71
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QY 181 KKKQFIE---KYNFDIVNDEPL-EGRYKWDRL 208
DB 176 LRNKLLECMKYNFDPEKDEPLGGGRYEWVKL 207

RESULT 14

AAAY44335
ID AAY44335 standard; protein; 191 AA.
XX
XX AAY44335;
AC
DT 29-FEB-2000 (first entry)
XX
DE Arabidopsis thaliana CDK inhibitor, ICK1.
XX
XX Cyclin-Dependent kinase inhibitor; CDK; Interactor of Cdc2 kinase 1;
KW ICK1; Cdc2a; D-class cyclin; CycD1; CycD2; CycD3; morphogenesis;
KW antisense construct; tissue-specific promoter; transgenic plant;
KW male sterility.
XX
OS Arabidopsis thaliana.
XX
XX Key Location/Qualifiers
FH Region 109..153
FT /note= "Important for interaction with CycD3"
XX
XX WO9964599-A1.
PN
PD 16-DEC-1999.
XX
XX 08-JUN-1999; 99WO-CA000532.
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XX 08-JUN-1998; 98CA-02235978.
PR 31-DEC-1998; 98CA-02256121.
XX
XX (MTAC) AGRIC & AGRIFOOD CANADA.
PA (UYSA) UNIV SASKATCHEWAN TECHNOLOGIES INC.
PA (CANA) NAT RES COUNCIL CANADA.
XX
PI Wang H, Powke LC, Crosby WL;
XX
DR WPI: 2000-097540/08.
DR N-PSDB; AAZ29415.
XX
XX Modifying plant cell development using nucleic acid encoding inhibitor of
PT cyclin-dependent kinase, or corresponding antisense sequence, e.g. for
PT inducing male sterility.
XX
XX Claim 7; Fig 1; 58pp; English.
XX
XX The present sequence is A. thaliana Cyclin-Dependent kinase (CDK)
CC inhibitor, ICK1. Interactor of Cdc2 kinase 1 (ICK1) interacts with Cdc2a,
CC D-class cyclins, CycD1, CycD2 and CycD3. Growth, morphogenesis,
CC multiplication, enlargement, differentiation and maturation of plant
CC cells can be modified by transforming them with nucleic acid encoding CDK
CC inhibitor or antisense construct complementary to the CDK inhibitor gene,
CC operably linked to a tissue-specific promoter. The transgenic plants
CC exhibit alteration of traits such as petals, male sterility and ability
CC to set seeds
XX
XX Sequence 191 AA;
Query Match 16.8%; Score 175.5; DB 3; Length 191;
Best Local Similarity 26.7%; Pred. No. 6.8e-07;
Matches 59; Conservative 34; Mismatches 63; Indels 65; Gaps 9;
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DB 7 KAKGIVEAGVSGSTYMLRSRR-----IVYRSEKS-----SSVSV 41
QY 76 GGEESDQSSSTSSGCTFSESKEIAKNSSFGVDLEDHQIETETSTF-----ITSNF 128
DB 42 VGD-----NGVSSSC--SGSNEYKKEL---IHLEEDKDGDTETSTYRGTKKLFENL 91
QY 129 RKE-----TSPVSEGL-----GETTMESSATKQPGVKTPTAAE 167

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OM protein - protein search, using sw model

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(without alignments)
577.839 Million cell updates/sec

Title: US-09-980-758A-8

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/prodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/1aa/PCITUS_COMB.pep.*
6: /cgn2_6/prodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	177	16.9	229	4	US-09-526-597D-2
2	152	14.5	222	4	US-09-526-597D-4
3	136.5	13.1	223	4	US-09-526-597D-6
4	133.5	12.8	327	4	US-09-526-597D-34
5	132.5	12.7	414	1	US-07-667-276A-4
6	128	12.2	2137	3	US-09-134-001C-4463
7	121.5	11.6	286	4	US-09-248-796A-22818
8	116.5	11.1	312	4	US-09-270-767-33271
9	116.5	11.1	312	4	US-09-270-767-48488
10	116	11.1	402	4	US-09-248-796A-18910
11	114.5	11.0	414	4	US-09-248-796A-19046
12	113	10.8	669	4	US-09-107-532A-6532
13	112.5	10.8	491	4	US-09-107-532A-6115
14	111	10.6	699	4	US-09-248-796A-23200
15	110.5	10.6	685	4	US-09-248-796A-20197
16	109.5	10.5	1306	4	US-09-538-092-330
17	107.5	10.3	165	4	US-09-248-796A-23180
18	107.5	10.3	382	4	US-09-248-796A-17276
19	107	10.2	273	4	US-09-248-796A-25975
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21	106	10.1	145	3	US-08-808-599A-41
22	106	10.1	556	4	US-09-248-796A-22338
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25	104	10.0	161	3	US-09-134-001C-4577
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27	104	10.0	539	4	US-09-248-796A-16542

28	104	10.0	1857	4	US-09-917-254-91	Sequence 91, Appl
29	104	10.0	1372	4	US-09-538-092-1084	Sequence 1084, Ap
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34	103.5	9.9	633	4	US-09-248-796A-18023	Sequence 18023, A
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ALIGNMENTS

RESULT 1

US-09-526-597D-2
; Sequence 2, Application US/09526597D
; Patent No. 6710227

GENERAL INFORMATION:
; APPLICANT: De Veylder, Lieven

; APPLICANT: De Almeida, Janice

; APPLICANT: Landrieu, Isabelle

; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof

; FILE REFERENCE: 1187-2

; CURRENT APPLICATION NUMBER: US/09/526,597D

; CURRENT FILING DATE: 2000-03-16

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 209

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

US-09-526-597D-2

Query Match 16.9%; Score 177; DB 4; Length 209;
Best Local Similarity 30.7%; Pred. No. 5.1e-08;
Matches 65; Conservative 44; Mismatches 73; Indels 30; Gaps 13;

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DB	121	S-WIYDDLNK--SEESMMNDSSVAVDEVESRRRLKSLHETVKEAELEDFQVASK--D	175
QY	181	KKKQIE---KYNFDIVNDEPL-EGRYKWRDL	208
DB	176	LRNKLLCSMKYNFDFEKDEPLGGGRYEWVKL	207

RESULT 2

US-09-526-597D-4
; Sequence 4, Application US/09526597D
; Patent No. 6710227

GENERAL INFORMATION:
; APPLICANT: De Veylder, Lieven

; APPLICANT: De Almeida, Janice

; APPLICANT: Landrieu, Isabelle

; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof

```
; FILE REFERENCE: 1187-2
; CURRENT APPLICATION NUMBER: US/09/526,597D
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-526-597D-4

Query Match      14.5%; Score 152; DB 4; Length 222;
Best Local Similarity 30.6%; Pred. No. 9.1e-06;
Matches 59; Conservative 24; Mismatches 70; Indels 40; Gaps 11;

QY 16 RKRLAEASSTSPFLKTKLNDSSDPSHDVIVFAVSSSVASSAALASDECSVTI 75
Db 62 KSRRL--EKPSLIEPKQPPRVHRSGIKESGRS--RVDVSNVSPVAQSS--NEDEC--- 112
QY 76 GGEESDQSSISGCGFTSESKEIAKNSSSGVVDLEDHQIETETETSTITSNFRKETSPV 135
Db 113 ----PDNFVSVQVSC-----GENSLGF-----ESRHSSTRESTPCNFV-----EDMEI 150
QY 136 SEGGETTTEMESSATK---RKQGVKRTPTAAEIEDLFSELESPPDDKKQKQFIKYNPD 192
Db 151 MVTGSGSTRSM--CRATKEYTREQDNV--IPTTSEMEEFFAYAE--QQQORLFWEKYNPD 204
QY 193 IVNDEPLEGRYK 205
Db 205 IVNDIPLSGRYEW 217

RESULT 3
US-09-526-597D-6
; Sequence 6, Application US/09526597D
; Patent No. 6710227
; GENERAL INFORMATION:
; APPLICANT: De Veylder, Lieven
; APPLICANT: De Almeida, Janice
; APPLICANT: Landrieu, Isabelle
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
; FILE REFERENCE: 1187-2
; CURRENT APPLICATION NUMBER: US/09/526,597D
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-526-597D-6

Query Match      13.1%; Score 136.5; DB 4; Length 223;
Best Local Similarity 23.5%; Pred. No. 0.00022;
Matches 54; Conservative 45; Mismatches 82; Indels 49; Gaps 10;

QY 11 KMSERKREAEASSTSPFLKTKLNDSSDPSHDVI-----VFAVSSS----- 58
Db 9 KSKSESPNSPTPTSPSPSPPTIT--TNSPPPTTNSDGVKTRTARTALENNQNQL 67
QY 59 SVASSA-----ALASDECSVTIGGEESDQSSISGCGFTSESKEIAKNSSSGFV 107
Db 68 SVSSDYLQLRNRRLKRLIRQHSAKRNGHDGNPKSPI--GDSIAEKTQKSPENPA 125
QY 108 DLEDHQIETETSTITSNFRKETSPV-----SEGLGE-----TTTEMESSATKQKPG 158
Db 126 EFKENAEDTERSA-----RETPVHLINRADVLPRPPIRTPTTEANPKTEQPT 176
QY 159 VRKTPAAEIEDLFSELESPPDDKKQKQFIKYNFDIVNDEPLEGRYKWDRL 208
Db 177 I---PISREFEFCAKHEA--EQQREFMEKYNFDPVTEQPLPGRYEWK 221

; FILE REFERENCE: 1187-2
; CURRENT APPLICATION NUMBER: US/09/526,597D
; CURRENT FILING DATE: 2000-03-16
; Patent No. 6710227
; GENERAL INFORMATION:
; APPLICANT: De Veylder, Lieven
; APPLICANT: De Almeida, Janice
; APPLICANT: Landrieu, Isabelle
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
; FILE REFERENCE: 1187-2
; CURRENT APPLICATION NUMBER: US/09/526,597D
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-526-597D-34

Query Match      12.8%; Score 133.5; DB 4; Length 327;
Best Local Similarity 20.2%; Pred. No. 0.00067;
Matches 57; Conservative 45; Mismatches 79; Indels 101; Gaps 11;

QY 1 PRDLP-----KNPREKMSERKERELAEAS-----TSFSPKTKTKL 37
Db 71 PSSLPPTSASPNPPSKQKMKKQKQMDGCVLQLRSRRLQKPPVIVIRSTKRRKQRR 130
QY 38 NDSDSDSPDSDHVIIVFAVSSSVASSAALASDECSVTIGGEESDQSSISGCGFTSESKE 97
Db 131 NETGRNPNSR-----NLDISIRGDSRSVSSESVVFGKDKDLISEIN----- 174
QY 98 IAKNSSSFG-----VDLEDHQIET---ETETSTITSNFRKE--TSPVSEG-----LGTTT 144
Db 175 ---KDTFGQNFDFLEEHQTSFNRTRSTPCSLIRPEIMTTPGSGTKLNICVSESNQ 231
QY 145 EMESSATKQKQGVKRTPTAAEIEDLFSELESPPDDKKKQKFIK----- 188
Db 232 REDSLRSRSHRR-----PTTPMEDPEFSGAE--EEQKQKFIKVFPRFICSVLLVMSF 283
QY 189 -----YNFDIVNDEPLEGRYKWDRL 208
Db 284 QFVLFFSGLVSLMVSNVSNFFRYNFDVPVNEQPLPGRFEMTKV 325

RESULT 5
US-07-667-276A-4
; Sequence 4, Application US/07667276A
; Patent No. 5470971
; GENERAL INFORMATION:
; APPLICANT: Kondo, Keiji
; APPLICANT: Inouye, Masaori
; TITLE OF INVENTION: STRESS-INDUCED PROTEINS, GENES CODING
; TITLE OF INVENTION: THEREFOR, TRANSFORMED CELLS OF ORGANISMS, METHODS AND
; TITLE OF INVENTION: APPLICATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weiser & Associates
; STREET: 230 S. Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/667,276A
; FILING DATE: 11-MAR-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
```



```
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 377,5351P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-667-276A-4

Query Match      12.7%; Score 132.5; DB 1; Length 414;
Best Local Similarity 29.3%; Pred. No. 0.0011;
Matches 61; Conservative 25; Mismatches 73; Indels 49; Gaps 9;

QY 7 NPREKMSERKRLAEASSTSFPLKTKKLNDSDDSPDHDVIVFAVSSSVASSAAL 66
Db 10 NKKEVKASQAKK--EKAVSSS-----SSSSSSS-----SSSESESE 50

QY 67 ASDECSVTIGGERSDQSSISGCFITSES-----KEIAKNSSSGFVD-LEDHQIETET 120
Db 51 SESESSSSSSSDSSSSSSSS---DSEAEFTKKEEKDSSSSSDSSDSEDEEEKEE 107

QY 121 STFITNFRKETSVPSEGLGETTEMESSATKRKQGVKKTPTAAAEIEDLFELESPPD 180
Db 108 TKKEESKSSSSDSSSSSSSDSEKEESNDKKRS-----EDABEEDEESS 155

QY 181 KKKQFIKYNFDIVNDP---LEGRYKW 205
Db 156 NKKQKNEE-----TEEPATIFVGRLSW 177

RESULT 6
US-09-134-001C-4463
; Sequence 4463, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4463
; LENGTH: 2137
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4463

Query Match      12.2%; Score 128; DB 3; Length 2137;
Best Local Similarity 25.6%; Pred. No. 0.027;
Matches 45; Conservative 35; Mismatches 66; Indels 30; Gaps 6;

QY 24 ASSTSFPLKTKKLNDS-----SDSPDHDVIVFAVSSSVASSAALASDE 70
Db 1868 SASTSLSGSTSVSDSTSTSTASASTSDESDDASTSLGSGSTSIISDSTSTSD 1927

QY 71 CSVTIGGERSDQSSISGCFITSESKEIAKNSSFGVDLEDHQIETETSTFTSNFRK 130
Db 1928 SASTSTSESASTSVSES--DSESTSVSESST-----SVSDSTSTST---TSESAS 1974

QY 131 ETPSVSEGLGETTEMESSATKRKQGVKKTPTAAAEIEDLFELESPPDKKKQFI 186
Db 1975 TSTSESESTSESTSVSESSTSIISDS---SSTSTSMSTSETFTIS--QSPINSESQFI 2026
```

RESULT 7

```
US-09-248-796A-22818
; Sequence 22818, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 22818
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-22818
```

```
Query Match      11.6%; Score 121.5; DB 4; Length 286;
Best Local Similarity 28.3%; Pred. No. 0.0065;
Matches 39; Conservative 27; Mismatches 61; Indels 11; Gaps 3;

QY 12 KMSERKRLAEASSTSFPLKTKKLNDSDDSPDHDVIVFAV---SSSSVASSAALAS 68
Db 152 QQQSQSQSQSQSTSTSQAPLSTMSDNTSFVSPDSTLLVSAATTTSSSSSSSLTP 211

QY 69 DECSVTIGGERSDQ-----SSISGCFITSESKEIAKNSSFGVDLEDHQIETETSTFTI 124
Db 212 STSDVTSSASSSPSTSSSSSTAFSSSTTETSSATSSSTSSSILSTQNTSLSS 271

QY 125 TSNFRKETSPVSEGLGET 142
Db 272 NTSF-----SVSHGAGET 285
```

RESULT 8

```
US-09-270-767-33271
; Sequence 33271, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33271
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-33271
```

```
Query Match      11.1%; Score 116.5; DB 4; Length 312;
Best Local Similarity 22.9%; Pred. No. 0.02;
Matches 49; Conservative 32; Mismatches 94; Indels 39; Gaps 6;

QY 20 LAEASSTSFPLKTKKLNDSDDSPD-----SHDVIVFAVSSSVSA 61
Db 6 LSSDSTDTAATAASDNTDITTDGSTDSTDCGSSNASTEGSEGEDTTISTESSGSTE 65

QY 62 SSAALASDECSVTIGGERSDQSSISGCF-----TSESKEIA-KNSSSFGVDLEDHQ 113
Db 66 STDALASDG-STTEGSTVEDLSSSTSDVTSDSTITDSSPSTEVSGSTSSSDTGSSTD 124

QY 114 IETETSTFTITSNFRKETSPVSEGLGET-----TTEMESSATKRKQGVKKTPT 164
Db 125 ASSTASSTDVTES---TDSVTSGGSTDTTESGPTTESTTEGSTTGSTDSTQSTDL 181
```

```

Qy 165 AAIEDLFSELESPDDKKQFIEKYNFDIWNDEP 198
      : | : | : | : | : | : | : | : | : | : | : | : |
Db 182 DSTSDIWTSDKODESESSSTPYSFDSVTKSKP 215

```

RESULT 9

```

US-09-270-767-48488
; Sequence 48488, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48488
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-48488

```

Query Match	11.1%	Score 116.5;	DB 4;	Length 312;
Best Local Similarity	22.9%	Pred. No. 0.02;		
Matches	49;	Conservative	32;	Mismatches 94;
				Indels 39;
				Gaps 6;

[illegible]

Qy	62	SSAALASDEC	SVTIGGERSDQSSISSGCF-----TSEKETA-KNSSSFGVLEDHQ	113
		:	:	:
		:	:	:
Db	66	STDAIASDG-	STTEGSGTVEDLSSTSSDVTSDSNTDSSPSTVGSGTSSSSSDGSSST	124
		:	:	:
		:	:	:

Qy	114	IETETETFTITNFRKETSPVSEGLGT-----TTEMSSSATKKQPGVRKTP	164
D6	125	ASSTEASGTDVTEF--TDSTVSGGTSDFTEESGTEESTTEGSTTSGDSTQD	181

Qy	165	A	A	E	D	L	F	S	E	L	E	S	P	D	D	K	K	Q	F	I	E	K	Y	N	F	D	I	V	N	D	E	P	198
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:		
Db	182	D	S	T	S	I	D	I	W	S	T	K	D	D	E	S	S	T	P	S	F	D	S	E	V	T	K	S	P	215			

RESULT 10

US-09-248-796A-18910
; Sequence 18910, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18910
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18910

Query Match	11.1%;	Score 116;	DB 4;	Length 402;
Best Local Similarity	29.3%;	Pred. No. 0.032;		
Matches	53:	Conservative	25:	Mismatches 61:
				Indels 42:
				Gaps 7:

Qy 10 EKMSERKRE-----LAEASSTSFSP LKTKLNDSSDPDSDHVDVFAVSSSS 59
:|:|:|:| | :|:|:| | :|:|:| | :|:|:| |

[illegible]

Query Match	11.0%;	Score 114.5;	DB 4;	Length 414;
Best Local Similarity	21.4%;	Pred. No. 0.045;		
Matches 48;	Conservative	51;	Mismatches 92;	Indels 33;
				Gaps 6;

QY	2	RDLPK-----	-----NPREKMWSEKRELAEEASTSFSLPKTKTKLNDSSDSSPSHD	49
		:::::	:::::	
DB	95	KELPKFKQLEGIID	VENQEKKKKPRN-----SSSDSDYSESESESTDSSESSSSSDS	150
		:::::	:::::	

Qy	50	VIVFAVSSSVASSAALASDECSVTTCGE--ESDQSSSISSCCFTSSEKIAKNSSSFGV	107
Dq	151	FGSDSSSSSSSSSSSSSSDSDDEEDKDEAKENKSDSENSEKVEEDNKDTSDDSS	210

QY	108	DIEDHQTETETSTFTISNFKETSPVSEGLGETITEMES----	SSATKRQPGVRKT	162
		: : : : : : : : : : : : : : : : : : : : :		
DB	211	SSSDSKYDSSSSSSSYDYDYDYDSSRSDSYDSSSYDSSSDSDSDSDSDSS	SDSDSDSDSDSS	270

```
QY      163 PTAAEIDLFSELES-----PDDKKQFIEKYNFDVNDLEPL 200
       :::|::||::||::||::||::||::||::||::||::||::
Db      271 ESSSEDSSSSSSESKEEQPEDKKR---KHTDIDIKEEKDKVK 310
```

RESULT 12

US-09-107-532A-6532
; Sequence 6532, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA

```

, ZIP: 02354
,
, COMPUTER READABLE FORM:
, MEDIUM TYPE: CD/ROM ISO9660
, COMPUTER: PC
, OPERATING SYSTEM: <Unknown>
, SOFTWARE: ASCII
,
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/09/107,532A
, FILING DATE: 30-Jun-1998
,
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: 60/085,598
, FILING DATE: 14 May 1998
, APPLICATION NUMBER: 60/051571
, FILING DATE: July 2, 1997
,
, ATTORNEY/AGENT INFORMATION:
, NAME: Ariniello, Pamela Deneke
, REGISTRATION NUMBER: 40,489
, REFERENCE/DOCKET NUMBER: GTC-012
,
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: (781)893-5007
, TELEFAX: (781)893-8377
,
, INFORMATION FOR SEQ ID NO: 6532:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 669 amino acids
, TYPE: amino acid
, TOPOLOGY: linear
, MOLECULE TYPE: protein
, HYPOTHEetical: YES
, ORIGINAL SOURCE:
, ORGANISM: Enterococcus faecium
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: (B) LOCATION 1...669
, SEQUENCE DESCRIPTION: SEQ ID NO: 6532:
US-09-107-532A-6532

```

Query Match	10.8%;	Score 113;	DB 4;	Length 669;
Best Local Similarity	23.8%;	Pred. No. 0.12;		
Matches	43;	Conservative 35;	Mismatches 87;	Indels 16; Gaps 5;
QY	7	NPEKKMWRKRRLAEAEASSTFSPCLKTKLNDSSDSSPDSDHVDIVFAVSSSSVASSA--	64	
Db	351	DPENEIFISDNGTDTTTSSTDTSS-----TTSDDSSDSSSTSSDSDTSTSTSDTSTSDTSASS	405	
QY	65	-----ALASDECSTVIGGEESQSSISGCGTTSSEKEIAKNSSSGFVDLEHQIETET	118	
Db	406	DSDTDTTSTSDTSDTSSASSDSDTGTSTSDTSDTSSD--SDTSTSTSDTSDTSDTSASSDS	464	
QY	119	ETSTFTSTNFRKETSVPSEGLGCTTTEMESSSATKKQPGVKRTPPTAAELEDLFSELESP	178	
Db	465	TDSTSTSD--SDTSSASSDST--DTTSTSDTSDTSDTSASSDSDTSTSTSDTSDTSDTSASSDST	522	
QY	179	D	179	
Db	523	D	523	

```

RESULT 13
US-09-107-532A-6115
; Sequence 6115, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354

```

COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
FILING APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
FILING APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinieglo, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6115:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...491
SEQUENCE DESCRIPTION: SEQ ID NO: 6115:
US-09-107-532A-6115

Query Match	10.8%;	Score 112.5;	DB 4;	Length 491;
Best Local Similarity	27.1%;	Pred. No. 0.085;		
Matches	49;	Conservative 35;	Mismatches 62;	Indels 35; Gaps 8
QY	19	ELAEHASSYFSFLKKTKLNDSSDPDSDHVI VFAVSSSV-----ASSAALASDECSTVI	75	
DB	42	KTAKETET-----TEMS-NDVTAESSELLTTSSSESSTTNAESSTTSSSESSTTS	93	
QY	76	GGEESDQSSISGGCTTSKSKIAKSSSPGVLDLHQIETETSTFTITGNFRKETSPV	135	
DB	94	NAESSTTSSSESS---TTSNAESSTTSSSESSSTTSSTSSSTTSITSS--KVTKP-	147	
QY	136	SEGLGTTTMEWSSATKRPQGVKTKPTAAIEDLFSELESPPDKKKQFI-----EKYNF	191	
DB	148	-----NHIESKKKAPTEGQTKTFTPO-----QIETSEFSQOPILSGNEEIH	193	
QY	192	D	192	
DB	194	D	194	

```

RESULT 14
US-09-248-796A-23200
; Sequence 23200, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 23200

```

```

; LENGTH: 699
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (487),(699)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-248-796A-23200

Query Match      10.6%; Score 111; DB 4; Length 699;
Best Local Similarity 21.6%; Pred. No. 0.19;
Matches 46; Conservative 38; Mismatches 61; Indels 68; Gaps 7;

QY      3  DLKPNPREKKMGSRERKELAEASSTSTSPPLKTKLNDSSDSDSHDVIVFAVSS 57
DB      411  DKQSP-----KRVSDQASSNQEIVDNPTATKISESSSEEE-----I 451

QY      58  SSVASSAALASDECSTVTGGESDQSSISGCGFTTSKEIAKNSSSFGVDL---EDHQI 114
DB      452  ANNPTPTMDIDESSSSGEEEMASNTSKVDSGASXNDKEVANNPTKVSDGLASSNDEEI 511

QY      115  ETETETSTFI----TSNFKETSPVSEGLGETTTEMESSAT-----KKQP----- 157
DB      512  SNNPETLTKVSDSSSSDEEASDVAVMDGTSGSDTSTSTNPTPPKLNQKQPIANAG 571

QY      158  -----GVRKTPATAA 166
DB      572  GDKVSNKSEIMVAPLPIATPRVQGLALTPTAS 604

RESULT 15
US-09-248-796A-20197
; Sequence 20197, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20197
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-20197

Query Match      10.6%; Score 110.5; DB 4; Length 685;
Best Local Similarity 25.6%; Pred. No. 0.2;
Matches 44; Conservative 32; Mismatches 73; Indels 23; Gaps 5;

QY      14  SERKREL-----AERASSTSPGLKTKLNDSSDSDSHDVIVFAVSSS-----VASSA 64
DB      71  SEQRSSIPIMSSDSESSERSSIGTILSESSDSIPTFFTRYWSPGMSRHYTNSTE 130

QY      65  ALASDECSTVTIGGESDQSS-----SISGCGFTTSKEIAKNSSSFGVDLEDHQIETET 120
DB      131  TLVSDVLLSSVAGDTSSESSVSIVSESSSVTSSES--VASESVTAVSIDSLYTTSEVVS 188

QY      121  -----STFTTSNFKETSPVSEGLGETTTEMESSSATKPKQGVKTKPT 164
DB      189  TSDSKIVPSTVPSPSEQRSSIPIMSSDSESSERSSSGTILSEENSDSIPT 240

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Search completed: September 30, 2005, 11:36:35
Job time : 28 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2005, 11:32:43 ; Search time 411 Seconds
(without alignments)
211.093 Million cell updates/sec

Title: US-09-980-758A-8
Perfect score: 1045
Sequence: 1 PRLPKNPREKMKSERKREL.....NFDVNDPELEGRYKWDRLX 209

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1846076 seqs, 415116000 residues

Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
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2: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1007	96.4	212	9 US-09-733-507-12	Sequence 12, Appl
2	1007	96.4	212	15 US-10-451-139-11	Sequence 11, Appl
3	969	92.7	196	15 US-10-451-139-22	Sequence 22, Appl
4	351.5	33.6	207	15 US-10-451-139-12	Sequence 12, Appl
5	346.5	33.2	195	15 US-10-451-139-23	Sequence 23, Appl
6	341	32.6	208	9 US-09-733-507-13	Sequence 13, Appl
7	210.5	20.1	176	15 US-10-424-599-212181	Sequence 212181,
8	177	16.9	46	17 US-10-890-629-59	Sequence 59, Appl
9	177	16.9	209	15 US-10-688-291-2	Sequence 2, Appl
10	177	16.9	209	15 US-10-451-139-19	Sequence 19, Appl
11	176.5	16.9	191	9 US-09-733-507-10	Sequence 10, Appl

12	175.5	16.8	191	9 US-09-733-507-2	Sequence 2, Appl
13	175.5	16.8	191	15 US-10-451-139-2	Sequence 2, Appl
14	172	16.5	205	15 US-10-424-599-182928	Sequence 182928,
15	171.5	16.4	224	15 US-10-424-599-210190	Sequence 210190,
16	168.5	16.1	196	9 US-09-733-507-16	Sequence 16, Appl
17	168.5	16.1	196	15 US-10-451-139-15	Sequence 15, Appl
18	162.5	15.6	189	15 US-10-451-139-17	Sequence 17, Appl
19	159	15.2	276	9 US-09-733-507-11	Sequence 11, Appl
20	159	15.2	176	15 US-10-451-139-10	Sequence 10, Appl
21	155	14.8	222	15 US-10-451-139-21	Sequence 21, Appl
22	153.5	14.7	217	16 US-10-425-115-254155	Sequence 254155,
23	153.5	14.7	217	17 US-10-890-629-4	Sequence 4, Appl
24	153.5	14.7	255	15 US-10-425-114-61054	Sequence 61054, A
25	153	14.6	262	15 US-10-333-006-10	Sequence 10, Appl
26	153	14.6	417	16 US-10-437-963-195115	Sequence 195115,
27	152	14.5	222	15 US-10-688-291-4	Sequence 4, Appl
28	150.5	14.4	137	15 US-10-451-139-13	Sequence 13, Appl
29	149	14.3	194	15 US-10-333-006-44	Sequence 44, Appl
30	149	14.3	194	16 US-10-437-963-120870	Sequence 120870,
31	148	14.2	213	17 US-10-890-629-2	Sequence 2, Appl
32	148	14.2	248	15 US-10-425-114-59718	Sequence 59718, A
33	147.5	14.1	137	9 US-09-733-507-14	Sequence 14, Appl
34	144.5	13.8	212	16 US-10-425-115-268129	Sequence 268129,
35	141.5	13.5	205	15 US-10-424-599-235800	Sequence 235800,
36	138.5	13.3	225	16 US-10-437-963-198574	Sequence 198574,
37	138.5	13.3	406	16 US-10-451-467A-262	Sequence 262, App
38	136.5	13.1	223	15 US-10-688-291-6	Sequence 6, Appl
39	135.5	13.0	95	16 US-10-767-701-36263	Sequence 36263, A
40	134	12.8	218	16 US-10-437-963-128205	Sequence 128205,
41	134	12.8	254	17 US-10-890-629-12	Sequence 12, Appl
42	134	12.8	256	9 US-09-993-308-2	Sequence 2, Appl
43	134	12.8	256	11 US-09-993-808B-2	Sequence 2, Appl
44	133.5	12.8	252	16 US-10-425-115-223026	Sequence 223026,
45	133.5	12.8	327	15 US-10-688-291-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-09-733-507-12
; Sequence 12, Application US/09733507
; Patent No. US20010025379A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan
; TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth
; TITLE OF INVENTION: Regulators
; FILE REFERENCE: 81601-3
; CURRENT APPLICATION NUMBER: US/09/733,507
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: CA 2,256,121
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 12
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-733-507-12

Query Match	96.4%	Score 1007;	DB 9;	Length 212;
Best Local Similarity	99.5%	Pred. No. 1.7e-68;		
Matches 202;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	6	KNPREKMKSERKRELAEASSTSFPLKTKLNDSSDSDSPDSDHDVIVFAVSSSVASSAA	65	
DB	10	KNPREKMKSERKRELAEASSTSFPLKTKLNDSSDSDSPDSDHDVIVFAVSSSVASSAA	69	
QY	66	LASDSCSVTIGGEESDQSSISGGCFTSESKIAKNSSFGVDLEDHQHQTETETSTFTT	125	
DB	70	LASDSCSVTIGGEESDQSSISGGCFTSESKIAKNSSFGVDLEDHQHQTETETSTFTT	129	
QY	126	SNFRKETSPVSEGLGETTTESSATKRKOPGVKRTPTAAEIEDLFSELESPDDKKQF	185	

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Db 130 SNFRKETSFSVSEGLGTTTMESSATKRKQPGVRKTPATAAEIEDLFSELESQDDKKQF 189
Qy 186 TEKYNFDIVNDEPLGRYKWDRL 208
Db 190 TEKYNFDIVNDEPLEGRYKWDRL 212

RESULT 2
US-10-451-139-11
; Sequence 11, Application US/10451139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: WANG, HONG
; APPLICANT: ZHOU, YONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-451-139-11

Query Match 96.4%; Score 1007; DB 15; Length 212;
Best Local Similarity 99.5%; Pred. No. 1.7e-68;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 KNPREKKMSERKRELAERASTSFSPCLKTKLNDSSDPSHDVIVFAVSSSVASSAA 65
Db 10 KNPREKKMSERKRELAERASTSFSPCLKTKLNDSSDPSHDVIVFAVSSSVASSAA 69

Qy 66 LASDCSVTIGEEESQSSISGCGFTSESKEIAKNSSSFGVDLEDHQIETETSTFIT 125
Db 70 LASDCSVTIGEEESQSSISGCGFTSESKEIAKNSSSFGVDLEDHQIETETSTFIT 129

Qy 126 SNFRKETSFSVSEGLGTTTMESSATKRKQPGVRKTPATAAEIEDLFSELESQDDKKQF 185
Db 130 SNFRKETSFSVSEGLGTTTMESSATKRKQPGVRKTPATAAEIEDLFSELESQDDKKQF 189

Qy 186 TEKYNFDIVNDEPLGRYKWDRL 208
Db 190 TEKYNFDIVNDEPLEGRYKWDRL 212

RESULT 3
US-10-451-139-22
; Sequence 22, Application US/10451139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: WANG, HONG
; APPLICANT: ZHOU, YONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
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; PRIOR APPLICATION NUMBER: US 60/255,908
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-451-139-22

Query Match 92.7%; Score 969; DB 15; Length 196;
Best Local Similarity 99.5%; Pred. No. 1.2e-65;
Matches 195; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 MSERKRELAERASTSFSPCLKTKLNDSSDPSHDVIVFAVSSSVASSAAASDECS 72
Db 1 MSERKRELAERASTSFSPCLKTKLNDSSDPSHDVIVFAVSSSVASSAAASDECS 60

Qy 73 VTIGEEESQSSISGCGFTSESKEIAKNSSSFGVDLEDHQIETETSTTITSNFRKET 132
Db 61 VTIGEEESQSSISGCGFTSESKEIAKNSSSFGVDLEDHQIETETSTTITSNFRKET 120

Qy 133 SPVSEGLGTTTMESSATKRKQPGVRKTPATAAEIEDLFSELESQDDKKQFIEKYNFD 192
Db 121 SPVSEGLGTTTMESSATKRKQPGVRKTPATAAEIEDLFSELESQDDKKQFIEKYNFD 180

Qy 193 IVNDEPLEGRYKWDRL 208
Db 181 IVNDEPLEGRYKWDRL 196

RESULT 4
US-10-451-139-12
; Sequence 12, Application US/10451139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: WANG, HONG
; APPLICANT: ZHOU, YONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-451-139-12

Query Match 33.6%; Score 351.5; DB 15; Length 207;
Best Local Similarity 44.5%; Pred. No. 8.4e-19;
Matches 93; Conservative 30; Mismatches 57; Indels 29; Gaps 10;

Qy 9 REKKMSERKRELAERASTSFSPCLKTKLNDSSD--SSPDSDHDVIVFAVSSSVASSAAAL 66
Db 11 REMSETPKRUSEYEGSN-----IKRWRLDDDDVILKSPTR-----TLSSSSSSSLAYS 59

Qy 67 ASDE---CSVTIGEEESQ--SSISGCGFTSESKEIAKNSSSFGVDLEDHQIETETST 122
Db 60 VSDSGGFCVALSEEDDHLSSISGCGSSETNEIATRLPF--SDLEAHEI-SETEIST 116

Qy 123 FITSNFRKETSFSVSEGLGET-----TTEMESSATKRKQPGVRKTPATAAEIEDLFSELE 176
Db 117 LLTNNFRKQIGISSSENLTGETAEMDSATTEMRDQRKTEKKK-MEKSPTQAEILDFFSAE 175
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QY 177 SPDDKKQFIEKYNFDIVNDEPLEGRYKW 205
Db 176 RYE--QKRFTKYNYDIVNDTPLEGRYQW 202

RESULT 5

US-10-451-139-23
; Sequence 23, Application US/104511139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: WANG, HONG
; APPLICANT: ZHOU, YONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-451-139-23

Query Match 33.2%; Score 346.5; DB 15; Length 195;
Best Local Similarity 45.4%; Pred. No. 1.9e-18;
Matches 93; Conservative 27; Mismatches 58; Indels 27; Gaps 10;
QY 13 MSERKRELAERASTSFSPDKTKLNDSSD--SSPDSDHVIIVFAVSSSSVASSAALAE 70
Db 1 MSETKPKRDSEYEG--SNIKMRLLDDDDVLRSPTR-----TLSSSSSSSSSLAYSVSDS 51
QY 71 ---CSVTIGGEESDQ--SSISGCGFTSESKEIAKNSSSGVDLEDHQIETETSTFTS 126
Db 52 GGCFCVSLSEEDDHLSSISGCGSSSEIATRLPF--SDLEAHEI-SETEISTLLTN 108
QY 127 NFRKETSPPVSEGLGET-----TTMESSSATKRKQGVKRTPTAAEIEDLFSELESPPD 180
Db 109 NFRKQGISSENIGETAEWDSATTEMRDQKTEKKK-MEKSPTQAELEDDFFSAERYE- 166
QY 181 KKKQFIEKYNFDIVNDEPLEGRYKW 205
Db 167 -QKRFTKYNYDIVNDTPLEGRYQW 190

RESULT 6

US-09-733-507-13
; Sequence 13, Application US/09733507
; Patent No. US20010025379A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan
; TITLE OF INVENTION: Cyclin Dependent Kinase Inhibitors as Plant Growth
; TITLE OF INVENTION: Regulators
; FILE REFERENCE: 81601-3
; CURRENT APPLICATION NUMBER: US/09/733,507
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: CA 2,256,121
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana

US-09-733-507-13

Query Match 32.6%; Score 341; DB 9; Length 208;
Best Local Similarity 44.3%; Pred. No. 5.3e-18;
Matches 93; Conservative 30; Mismatches 57; Indels 30; Gaps 11;
QY 9 REKKMSERKRELAERASTSFSPDKTKLNDSSD--SSPDSDHVIIVFAVSSSSVASSAAL 66
Db 11 REMSETKPKRDSEYEGSN-----IKMRLLDDDDVLRSPTR-----TLSSSSSSSSSLAYS 59
QY 67 ASDE---CSVTIGGEESDQ--SSISGCGFTSESKEIAKNSSSGVDLEDHQIETETSTFTS 122
Db 60 VSDSGFCVSLSEEDDHLSSISGCGSSSEIATRLPF--SDLEAHEI-SETEIST 116
QY 123 FITSNFRKETSPPVSEGLGET-----TTMESSSATKRKQGVKRTPTAAEIEDLFSELES 175
Db 117 LUTNFRKQGISSENIGETAEWDSATTEMRDQKTEKKK-MEKSPTQAELEDDFFSAA 175
QY 176 ESPDDKKQFIEKYNFDIVNDEPLEGRYKW 205
Db 176 ERYE--QKRFTKYNYDIVNDTPLEGRYQW 203

RESULT 7

US-10-424-599-212181
; Sequence 212181, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 212181
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_33625C.1.pep
US-10-424-599-212181

Query Match 20.1%; Score 210.5; DB 15; Length 176;
Best Local Similarity 34.0%; Pred. No. 3.3e-08;
Matches 70; Conservative 28; Mismatches 67; Indels 41; Gaps 8;
QY 13 MSERKR-----ELAEASSTSFSPDKTKLNDSSDSDSDSDHVIIVFAVSSSSVASSAALA 67
Db 1 MGECKRCSLTIAAIEQPSSSQHSISKRTTAS-----FQLRSSDTQFPDTIV 48
QY 68 SDECSVTIGGEESDQSSISGCGFTSESKEIAKNSSSGVDLEDHQIETETSTFTS 123
Db 49 SPEASVSTG-----TVVSGDFCSDR---SCSSSHFKDL--HSVPSDLQTKGFQIVE 96
QY 124 -ITSNFRKETSPPVSEGLGETTTMESSSATKRKQGVKRTPTAAEIEDLFSELESPPDKK 182
Db 97 DSTNFRKFPFLLLSFSGDSEESAKSAAVRK-----LKTTPQAEIEEFAMAEKYE--R 149
QY 183 KQFIEKYNFDIVNDEPLEGRYKWDL 208
Db 150 KRFTEKYNFDIVDLPLEGRYQWRL 175

RESULT 8

US-10-890-629-59
; Sequence 59, Application US/10890629
; Publication No. US20050048624A1
; GENERAL INFORMATION:
; APPLICANT: Savidge, Beth

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Dd	42	VGD-----NGVSSSC--SGSNEYKKEL---IHLEEDKDGDTSTYRRGTRKLCENL 91 : : :
Qy	129	RKE-----TSPVSEGL-----GETTTMESSATKRKPQGVYRKTPTAAE 167 : : :
Dd	92	REEKEELSUKMENYSFEFAVKESLDCGCCGRKTMETVTVAEBEEKAKUMTEPTESE 151 : : :
Qy	168	IEDLFSELESDDKKQKIETYNFIDIVNDEPLEGYKWDRL 208 : : :
Dd	152	IEDFFVEAEK--QLKEKFKKYNFDFFEKEKPLEGRYEWVKL 190 : : :

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RESULT 12
US-09-733-507-2
; Sequence 2, Application US/097333507
; Patent No. US20010025379A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan
; TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth
; TITLE OF INVENTION: Regulators
; FILE REFERENCE: 81601-3
; CURRENT APPLICATION NUMBER: US/09/733,507
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: CA 2,256,121
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-733-507-2

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; PRIOR APPLICATION NUMBER: US 60/255,908
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-451-139-2

Query Match      16.8%; Score 175.5; DB 15; Length 191;
Best Local Similarity 26.7%; Pred No. 1.7e-05;
Matches 59; Conservative 34; Mismatches 63; Indels 65; Gaps

Qy 16 KRRLAEASSTSPFLKTKKLNDSDDSPSHDIVFAVSSSSVASSAALASDECSVTI 75
Db 7 KAKGIVEAGVSSTYQLRSRR-----IVVRSKSEK-----SSVSV 41

Qy 76 GGESDQSSSTSSCGFTSESKEIAKNSSSPGVDLEDHQIETETSTF-----ITSNF 128
Db 42 VGD-----NGVSSSC--SGSNEYKKEL---IHLEEDKDGDTSTYRRGTRKRLFENL 91

Qy 129 RKE-----TSPVSEGL-----GETTMESSSATKRQPGVRKKTPTAAE 167
Db 92 REBEKEELKSMENYSEFSAVKESLCCSCGRKTMEETVTAREEKAKLWTEMPTESE 151

Qy 168 IEDLFSELESPPDKKKQPIEKYNFDIVNDEPLEGRYKWDRL 208
Db 152 IEDFFVEAEK--QLKEKPKKYNFDFFEKEKPLEGRYEWVKL 190

RESULT 14
US-10-424-599-182928
; Sequence 182928, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 182928
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_136198C.1.pep
US-10-424-599-182928

Query Match      16.5%; Score 172; DB 15; Length 205;
Best Local Similarity 30.7%; Pred. No. 3.4e-05;
Matches 63; Conservative 36; Mismatches 74; Indels 32; Gaps 10

Qy 20 LAEASSTSPFLKTKKLNDSDDSPSHDIVFAVSSSSVASSAALASDECSVTIGGEE 79
Db 15 LAMEAVSSAEPSSKKKITSNTOEPK-----LSKTPRTSSSAVKPATVT-----E 61

Qy 80 SDQSSS---ISSGGFTSESKEI---AKNSSSFGVD-----LEDHQIET-ETETSTFTS 126
Db 62 MVQPSPEMVQORCLSPSTSSIPASCSSNSGIGLDQRIKLLDLEVASQVETSTCNGG 121

Qy 127 N--FRKETSPVSEGLGETTMESSSATKRQPGVRKT-PTAAEIEDLFSELESPPDKKK 183
Db 122 HEIERREMKRSSE-LRENSQPEPMEINSHRVLRSKAKAMPTETELEEFPFAASEK--DIQK 178

Qy 184 QFIKYNFDIVNDEPLEGRYKWDRL 208
Db 179 RFQDRYNDIVKQDVPLEGRYEWVOL 203

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RESULT 15
US-10-424-599-210190
; Sequence 210190, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 210190
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_3182C.1.pap
US-10-424-599-210190

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Query Match      16.4%; Score 171.5; DB 15; Length 224;
Best Local Similarity 30.9%; Pred. No. 4.1e-05;
Matches 42; Conservative 29; Mismatches 54; Indels 11; Gaps 4;

Qy 77 GEESDQSSISGCGFTSESKEIAKNSSFG---VDLEDHQIETETETSTFTTSNFRKETS 133
Db 94 GLASERDNLNHNKNDTLHENAEPQEAQSGFGENVLDFEGRERSTRESTPCSLIRSDTVRT 153

Qy 134 PVSEGLGETTTTMESSSATKQKQGVK-TPTAAEIEDLSELESPPDDKKQKQIEKYNFD 192
Db 154 P-----GSTTPTCSAEAYRTEHAARQIPTSRWDEFFAEIEAQOKK--FIEKYNFD 206

Qy 193 IVNDEPLEGRYKWDRL 208
Db 207 PVNEKPLSGRYEWKL 222

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Search completed: September 30, 2005, 11:43:33
Job time : 412 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2005, 10:08:22 ; Search time 24 Seconds
(without alignments)
837.888 Million cell updates/sec

Title: US-09-980-758A-8
Perfect score: 1045
Sequence: 1 PRDLPKNPREKKMSRKREL.....NFDIVNDEPLEGRYKWDRLX 209

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

- 1: Pir1:*
- 2: Pir2:*
- 3: Pir3:*
- 4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	346.5	33.2	195	2 H96532	hypothetical prote
2	177	16.9	209	2 T46140	hypothetical prote
3	175.5	16.8	191	2 T01132	cyclin-dependent k
4	168.5	16.1	196	2 T09968	cyclin-dependent k
5	156.5	15.0	500	2 S53785	nucleolar protein
6	138.5	13.3	406	2 S38170	SRP40 protein - ye
7	133.5	12.8	327	2 T00797	hypothetical prote
8	132.5	12.7	414	2 A39205	nuclear localizati
9	132.5	12.7	2271	2 F90073	hypothetical prote
10	121	11.6	536	2 T37544	hypothetical serin
11	120.5	11.5	1359	2 T34036	hypothetical prote
12	117.5	11.2	557	2 A96527	probable nuM1 prot
13	116.5	11.1	344	2 T40167	hypothetical prote
14	116.5	11.1	534	2 T39903	serine-rich protei
15	116	11.1	238	2 S77699	inner cell wall ma
16	116	11.1	1280	2 G96796	hypothetical prote
17	116	11.1	1312	2 T23088	vitellogenin I pre
18	113.5	10.9	611	2 T2456	hypothetical prote
19	113.5	10.9	1829	2 T24583	hypothetical prote
20	113	10.8	611	2 T06458	nucleolin homolog
21	113	10.8	916	2 S22864	DNA topoisomerase
22	112.5	10.8	725	2 A41258	a-aggutinin core
23	112	10.7	273	2 T44657	protein GP80 limpo
24	112	10.7	3507	2 T34513	hypothetical prote
25	111	10.6	1217	2 S52714	sericin1B - silkw
26	110.5	10.6	1224	2 F96795	hypothetical prote
27	109.5	10.5	581	2 T24555	hypothetical prote
28	109.5	10.5	888	2 T46726	secreted acid phos
29	109.5	10.5	1230	2 T22458	hypothetical prote

30	109.5	10.5	1306	2 S25370	MSB2 protein - yea
31	109	10.4	327	2 S48416	hypothetical prote
32	109	10.4	503	2 S63257	probable membrane
33	109	10.4	550	2 T29919	hypothetical prote
34	109	10.4	551	2 S64314	probable membrane
35	109	10.4	604	2 T15091	hypothetical prote
36	109	10.4	1063	2 D86731	hypothetical prote
37	109	10.4	1094	2 T50651	AP3-complex beta-3
38	108	10.3	4776	2 E95206	cell wall surface
39	107.5	10.3	667	2 A40713	cylicin I - bovine
40	107.5	10.3	1072	2 A86827	hypothetical prote
41	107.5	10.3	2748	2 S57976	nuclear migration
42	107	10.2	630	2 A39344	tumor-associated m
43	107	10.2	631	2 I52257	episialin - mouse
44	107	10.2	1015	2 JC6552	DNA topoisomerase
45	107	10.2	1234	2 T31623	hypothetical prote

ALIGNMENTS

RESULT 1

H96532
hypothetical protein F14J22.14 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H96532
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H96532
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-195 <STO>
A:Cross-references: UNIPROT:Q9FX90; GB:AE005173; NID:g10120423; PIDN:AAG13048.1; GSPDB: C:Genetics:
A:Gene: F14J22.14
A:Map position: 1

Query Match 33.2%; Score 346.5; DB 2; Length 195;
Best Local Similarity 45.4%; Pred. No. 3e-16;
Matches 93; Conservative 27; Mismatches 58; Indels 27; Gaps 10;

QY	13	MSERKRLAEASSTSFGLKTKLNDSD--SSPDSDHVI VFAVSSSSSVASSAALASDE 70
DB	1	MSETPKRDSVEG---SNIKRWLDDDDVLRSTR-----TLSSSSSSSLAVSVSDS 51
QY	71	---CSVTIGGEESDQ-SSSISSGCTFSKETAKNSSFGVDLEDHQIETETETFTITS 126
DB	52	GGFCSVALSEEDDHLSISSISGSCSSSTNEIATLPF--SDLEAHEI-SETEISTLLN 108
QY	127	NFRKETSVPSEGLGT-----TTMESSATKRPQGVKPTPTAAETEDLSELESPPD 180
DB	109	NFRKQGISSENGLGTAEMDSATTMRDQRKTEKKK-MEKSPTQALDFFSAAREY- 166
QY	181	KKQFIEKYNFDIVNDEPLEGRYKW 205
DB	167	-QKRFTKYNFDIVNDTLEGRYQW 190

RESULT 2

T46140
hypothetical protein T3A5.10 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

Qy	16	KRRLAEASSTSFSP	LKTKLNDSSDSSPD	SHDIVFAVSSSV	SSVAALASDECS	VTL	75
Db	7	KAKGIVAGVSST	WQLRSR-----	IVTVSEKS-----	SSVS	41	
Qy	76	GBESDQSSIS	SSCFTSESKEIA	KNSSSFGVLE	DHQIETETSTP	-----ITSN	128
Db	42	VGD-----	NGVSSC--SGS	NEYKKEL---IH	LEEDKGGTETST	YARGYRKLFENL	91
Qy	129	RKE-----	TSVSEGL-----	GETT	EMSSSATRKQP	QGVYRKPTAAE	167
Db	92	REEEKELSK	SMENYSSEF	ESAVKESL	DCCSGRKTMET	VTAAEEKAKL	TEMPTESE 151
Qy	168	IEDLFSELES	PDDKKKQFIE	KYNFDI	VNDEP	LEGYKWDR	L 208
Db	152	IEDFEVGA	EAK--QIK	EFPKKYN	DFD	FEKKEPL	LEGYEWVKL 190

RESULT 4
T09968
cyclin-dependent kinase inhibitor protein - red goosefoot
C/Species: *Chenopodium rubrum* (red goosefoot)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T09968
E/Fountain, M.D.; Krenz, A.; Beck, E.
submitted to the EMBL Data Library, November 1997
A/Description: A plant G1 cyclin-dependent kinase inhibitor gene from a photoautotrophic cyanobacterium.
A/Reference number: 216910

Query Match	16.1%	Score 168.5	DB 2	Length 196
Best Local Similarity	27.0%	Pred. No. 0.00019		
Matches	60	Conservative 32	Mismatches 63	Indels 67
Gaps	10			
Qy	20	LAEEASSTFRPLKTKTKLNDSSD-----SSPDGHDVIVFVSSSSVASSAAL	66	
Db	1	MAAAATPIS-SPAKIKKVSXSYNIPOLRGRKNLSAPEN-----FALETTPLEVAAV	54	
Qy	67	ASDE-----CSVT--IGGESPOSSISSGCF---TSSEKKEIAKNSSSPGVLDLEHQIETYE	117	
Db	55	VEEBEVANCSSEVITTAARSDFPSPSCSNYDQLSSSEPEVVKDDGLGNRTADPEVES-	113	
Qy	118	TETSTFTSNFRKETSPPVSEGLGETTTEWESSSATKTKQ-----PGVKTKT-----P	163	
Db	114	-----GEASSQKQKSHRTEAREATKLDQDYPATKSTVOIKMP	151	
Qy	164	TAAEIEDLFSLESPDDKKKQFIEKYNFDIVNDEPLEGRYKW	205	
Db	152	SDSRIEFFFAVAK--DLOKRFSEKYNFDIVKDVPLKGRYDW	191	

A;Accession: S55785
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-500 <GUL>

A;Cross-references: UNIPROT:P41891; EMBL:Z48166; NID:g6632261; PIDN:CAA88179.1; PID:g6632261; R;VanHoy, R.W.; Wise, J.A. Curr. Genet. 29, 307-315, 1996
A;Title: Molecular analysis of a novel Schizosaccharomyces pombe gene containing two RNF
A;Reference number: S68083; MUID:96171513; PMID:8598051
A;Accession: S68087
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 374-407 <VAN>
R;Brown, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. submitted to the EMBL Data Library, September 1997
A;Reference number: Z21733
A;Accession: T37634
A;Status: preliminary; translated from GB/EMBL/DDBU
A;Molecule type: DNA
A;Residues: 1-338,'S',340-500 <BRO>
A;Cross-references: EMBL:Z99091; PIDN:CAB11772.1; GSPDB:GN00066; SPDB:SPAC13F5.09
A;Experimental source: strain 972h-; coemid c13F5
C;Genetics:
A;Gene: gar2; SPDB:SPAC13F5.09
A;Map position: 1
C;Superfamily: ribonucleoprotein repeat homology
F;264-331/Domain: ribonucleoprotein repeat homology <RRM1>
F;367-433/Domain: ribonucleoprotein repeat homology <RRM2>

Query Match 15.0%; Score 156.5; DB 2; Length 500;
Best Local Similarity 29.5%; Pred. No. 0.0035;
Matches 57; Conservative 37; Mismatches 74; Indels 25; Gaps 6;

Qy 1 PRDLPKNPREKKMKRKLAEASSTFSPLKTKLNDSSDPDSDHVIYFAVSSSV 60
Db 64 PEPFKSVKKQKSKKKBESSSESSSESSSESSSESSSESSSESSSESSSESSSE 116
Qy 61 ASSAAALASDCSVTIGGEESDQSSSISSGCTSESKEIA-----KNSSSFGVDLEDH 114
Db 117 SSS-----SESEEVIVKTEKKSSSSSSSSSSSESESESESESESESSSS 173
Qy 115 ETETETSTFTTSNFR---KETSPVSEGLGTTTMMESSSATKRKQPGVARTPTAAIED 171
Db 174 ESESESSSSSE 228
Qy 172 FSELESPPDKKKQ 184
Db 229 -SESSSEDEKKRK 240

RESULT 6
SRP40 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YKR092C; protein YKR412a
C;Species: Saccharomyces cerevisiae
C;Date: 03-May-1994 #sequence revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: S38170; S40645; S37702
R;Baladron, V.; Ballesta, J.P.G.; Bou, G.; del Rey, F.; Esteban, P.F.; Garcia-Cantalejo, J. submitted to the Protein Sequence Database, March 1994
A;Reference number: S38158
A;Accession: S38170
A;Molecule type: DNA
A;Residues: 1-406 <BAL>
A;Cross-references: UNIPROT:P32583; EMBL:Z28317; NID:g486580; PID:g486581; MIPS:YKR092C
A;Experimental source: strain S288C
R;Bou, G.; Esteban, P.F.; Baladron, V.; Gonzalez, G.A.; Cantalejo, J.G.; Remacha, M.; Ji Yeast 9, 1349-1354, 1993
A;Title: The complete sequence of a 15 820 bp segment of Saccharomyces cerevisiae chromo
A;Reference number: S40644; MUID:94205265; PMID:8154186
A;Accession: S40645
A;Molecule type: DNA
A;Residues: 1-406 <BOU>
A;Cross-references: EMBL:X73541; NID:g450550; PIDN:CAA51946.1; PID:g450552
A;Experimental source: strain S288C
R;Lalo, D.; Carles, C.; Sentenac, A.; Thuriaux, P. submitted to the EMBL Data Library, May 1993
A;Description: Interactions between three common subunits of yeast RNA polymerases I and

QY 98 IAKNSSFG---VDLEDHQIET---ETETSTFITNFRKE--TSPVSESG-----LGTTTT 144
Db 175 ---KDTFGQNFLEEBHTQSFNRTRESTPCLIRPEINTTTPGSSTKLNICVSESNQ 231
QY 145 EMESSATKQPGVKYKPTAAEIEDLSELESPPDKKQFIETK-----188
Db 232 REDLSRSHRRR-----PTTPEMDEFFSGAE--EEQKQFIETKVFPFRFCISVLLVMSF 283
QY 189 -----YNFDIYNDEPLEGRYKWDRL 208
Db 284 QVLFESFCLVSLMVSNVSNFFRYNFDVNEQPLGRFETWKV 325
RESULT 8
A39205
nuclear localization sequence-binding protein NSR1 - yeast (Saccharomyces cerevisiae)
N/Alternate names: nucleolar protein NSR1; p67 protein; protein YGR159c;
C/Species: Saccharomyces cerevisiae
C/Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 09-Jul-2004
C/Accession: A39205; PC2395; S60450; S64468; S64470
R/Lee, W.C.; Xue, Z.; Melese, T.
J. Cell Biol. 113, 1-12, 1991
A/Title: The NSR1 gene encodes a protein that specifically binds nuclear localization se
A/Reference number: A39205; MUID:91177946; PMID:1706724
A/Accession: A39205
A/Molecule type: DNA
A/Residues: 1-414 <LEE>
A/Cross-references: UNIPROT:P27476; GB:X57185; NID:94057; PIDN:CAA40472.1; PID:g4058
R/Gamberi, C.; Contreas, G.; Romanelli, M.G.; Morandi, C.
Gene 148, 59-66, 1994
A/Title: Analysis of the yeast Nsr1 gene and protein domain comparison between Nsr1 and
A/Reference number: PC2395, MUID:95011659; PMID:7926838
A/Accession: PC2395
A/Molecule type: mRNA
A/Residues: 155-414 <GAM>
A/Cross-references: EMBL:X57185
A/Note: The authors translated the codon TTC for residue 188 as Arg, GGT for residue 254
R/Skala, J.; Nawrocki, A.; Goffeau, A.
Yeast 11, 1421-1427, 1995
A/Title: The sequence of a 27 kb segment on the right arm of chromosome VII from Sacchar
A/Reference number: S60435; MUID:96158062; PMID:8585325
A/Accession: S60450
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-414 <SKA>
A/Cross-references: EMBL:X85807; NID:g1045249; PIDN:CAA59817.1; PID:g1045265
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1995
R/Van Dyck, L.; Skala, J.; de Wergifosse, P.; Purnelle, B.; Talla, E.; Nawrocki, A.; Del
submitted to the Protein Sequence Database, May 1996
A/Reference number: S64428
A/Accession: S64468
A/Molecule type: DNA
A/Residues: 1-414 <VAN>
A/Cross-references: EMBL:Z72944; NID:g1323270; PIDN:CAA97173.1; PID:g243542; PID:g132327
A/Experimental source: strain S288C
R/Rieger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M.
submitted to the Protein Sequence Database, May 1996
A/Reference number: S64071
A/Accession: S64470
A/Molecule type: DNA
A/Residues: 1-188 <RIE>
A/Cross-references: EMBL:Z72944; MIPS:YGR159C
A/Experimental source: strain S288C
C/Genetics:
A/Gene: SGD:NSR1
A/Cross-references: SGD:S0003391; MIPS:YGR159C
A/Map position: 7R
C/Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotein
C/Keywords: DNA binding; nucleus; RNA binding
F.169-236/Domain: ribonucleoprotein repeat homology <RNM1>
F.268-336/Domain: ribonucleoprotein repeat homology <RNM2>

Query Match 12.7%; Score 132.5; DB 2; Length 414;
Best Local Similarity 29.3%; Pred. No. 0.11;
Matches 61; Conservative 25; Mismatches 73; Indels 49; Gaps 9;
QY 7 NPREKKMSERKRELAEEASSTSFSPCLKTKLNDSSDSPDSDHVDVFAVSSSSVASSAAL 66
Db 10 NKKEVKASKQKE--EKAKAVSS-----SSESSSS-----SSSSSESESE 50
QY 67 ASDECSVTIGGEESDQSSSISSGCFTSES-----KEIAKNSSSFGVD--LEDHQIETETET 120
Db 51 SESESSSSSSSDSESSSSSS--DSESEAEATKKEESKDSKSSSSSDSSDEEEEEEKEE 107
QY 121 STFITSNFRKETSVPSEGLGTTTTEMESSSATKKGQGVKPTPTAAEIEDLFSELESPPD 180
Db 108 TKKEESKSSSSSSSSSSSSDSESEKESNDKKRS-----EDAEEDDEDESS 155
QY 181 KKKQFIKYNFDIYNDEP---LEGRYKW 205
Db 156 NKKORNEE-----TEEPATIFVGRLSW 177
RESULT 9
P90073
hypothetical protein SA2447 [imported] - Staphylococcus aureus (strain N315)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: P90073
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: P90073
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-2271 <KUR>
A/Cross-references: UNIPROT:Q99QY4; GB:BA000018; PID:g13702612; PIDN:BAB43752.1; GSPDB:G
A/Experimental source: strain N315
C/Genetics:
A/Gene: SA2447
Query Match 12.7%; Score 132.5; DB 2; Length 2271;
Best Local Similarity 25.8%; Pred. No. 0.8;
Matches 47; Conservative 35; Mismatches 89; Indels 11; Gaps 4;
QY 14 SERKRELAEEASSTSFSPCLKTKLNDSSDSPDSDHVDVFAVS-----SSSVASSAALAS 68
Db 1024 SDKSMVSVVSSMSTSQSGTSESLSDSQSTSDSDSKLSLSSTSQSGTSTSTSTASVRT 1083
QY 69 DECSVTIGGEESDQSSSISSGCFTSESKEIAKNSSSFGVDLEDHQIETET----ETSTFI 124
Db 1084 SESQSTSGSMASQSDMSISTSFSDTSDSKASTASSEISQSASTSTSGSVSTSTSL 1143
QY 125 -TSNFRKETSVPSEGLGTTTTEMESSSATKKGQGVKPTPTAAEIEDL-FSELESPPDKK 182
Db 1144 STNSERTSTSVSDSTSLSTSESDISBSTSTSDSISSEISASESTSTSLSESNSTSDSE 1203
QY 183 KQ 184
Db 1204 SQ 1205
RESULT 10
T37544
hypothetical serine-rich protein - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T37544
R/McLean, J.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A/Reference number: Z21722
A/Accession: T37544

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A;Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-536 <MCL>  
A/Cross-references: UNIPROT:O13695; EMBL:Z99161; PIDN:CAB16206.1; GSPDB:GN00066; SPDB-SF:  
A:Experimental source: strain 972h-, cosmid c11c7  
C:Genetics:  
A/Gene: SPDB:SPAC11G7.01  
A/Map position: 1
```

Query Match 11.6%; Score 121; DB 2; Length 536;

Best Local Similarity 29.18; Pred. No. 0.86;

Matches 46; Conservative 24; Mismatches 54; Indels 34; Gaps 5;

Oy 24 ASSTFSPLKTKLNDDSDSPPSHDIVFAVSS---SVASSAALASDECVTIGERS 80
 :|||:|||:|||||:|||||:|||||:|||||:|
Db 58 SSGSSSSP-----LSGSFTSPASSSFITSLVSSSQOSSSSASLTSSSATLTSSSA 112

Oy 81 DQSSISGGCGTSESKEIAKNSSFGVDLE--DHOJETETETTF----- 123
 :|||:|||:|||||:|||||:|||||:|||||:|
Db 113 SPTSSSSHALLSSSSLVASSSGLHSSVPSSSSSYHSSMTTLGLSSAS 172

Oy 124 -ITSNPK-----ETSVPSEGLGETTEMES SAT 152
 :|||:|||:|||||:|||||:|||||:|||||:|
Db 173 IVGSTYRDGPSIILVTSIVSEVVPTTNWNSSS 210

RESULT 11

T34036
hypothetical protein B0041.7 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T34036
R/Fulton, R.; Wohldmann, P.
submitted to the EMBL Data Library, April 1997
A/Description: The sequence of C. elegans cosmid B0041.

A/Reference number: Z21466
A/Accession: T34036
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1359 <FUL>
A/Cross-references: UNIPROT:Q9U7E0; EMBL:AF000196; PIDN:AAC24256.1; GSPDB:GN00019; CEP:
A:Experimental source: strain Bristol N2; clone B0041
C:Genetics:
A/Gene: CESP:B0041.7
A/Map position: 1
A/Introns: 12/2; 59/2; 248/2; 582/1; 675/1; 733/3; 966/2; 1044/2; 1310/3

Query Match 11.5%; Score 120.5; DB 2; Length 1359;

Best Local Similarity 25.88; Pred. No. 2.7;

Matches 56; Conservative 33; Mismatches 85; Indels 43; Gaps 7;

Oy 3 DLKPMPREKKMSERKLAEASTPS-----PLKTKLNDDSSDPDS 47
 ||:::|||:|||||:|||||:|||||:|||||:|
Db 100 DRKKSXKVQDKKSKKTTSSEDDEEDEREQQKKKKTKTKQTSSSESSE 159

Oy 48 HDVIPAVSSSVASSAALADECSVTIGCESDOSSI-----SCFTS 93
 ::|||:|||||:|||||:|||||:|||||:|
Db 160 EEERVKVSNNKVESVKAET-----SEEDEDKPSKKKGGLKKAKSESSE 213

Oy 94 ESKEIAKN-SSSFGVDLEDHQIETET----ETSTFITSNFRKETSPVSEG LGTTTME 148
 :|||:|||:|||||:|||||:|||||:|||||:|
Db 214 DEEVKSKSKSKVVKVESESEDAEPKKKTEKRKSKTSSSESSESEKDSEEEKES 273

Oy 149 SSATKRQP-GVRKTPTAIEIDLFELESFPDDKKKQ 184
 :|||:|||:|||||:|||||:|||||:|||||:|
Db 274 SPEFKKKPLAVKLLSSDEESE--SDVELPOKKR 308

RESULT 12

A96527
probable nuMI protein [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear crease)
C/Date: 02-Mar-2001 #sequence revision 02-Mar-2001 #text change 09-Jul-2004

C/Accession: A96527
R/Theologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
C/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Lurob, J.S.; Maiti, R.; Marziani, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
C/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, K.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; MUID:21016719; PMID:11130712
A/Accession: A96527
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-557 <STO>
A/Cross-references: UNIPROT:Q9FVQ1; GB:AE005173; NID:gl1094815; PIDN:AAG29744.1; GSPDB: C/Genetics:
A/Gene: F2X7.6
A/Map position: 1

Query Match 11.2%; Score 117.5; DB 2; Length 557;
Best Local Similarity 24.9%; Pred. No. 1.5;
Matches 51; Conservative 27; Mismatches 70; Indels 57; Gaps 7;

Qy 1 PRDLPNPREKMSRKRELAEEASSTFSPLKK-----TKLNDSSDSSPD 46
Db 141 PAAAKXGVSVK---AKKESSEDDSSSEDEPAKKPAAKTAKPAKDDSSDDDDSDSDSD 197
Qy 47 SHDVIVFNVSSSVASALASDECSTVTGGESDQSSISSCGFTSESKEIAKNSSSFG 106
Db 198 EKPAATKAAAPAAAKAASSDSDSDS-----DEEDEDKPAKKADTKASK--KSSSDS 250
Qy 107 VLEHDHQIETETSTFTTSNPKETSPVSEGLGTTTWESSSATKRPQGVKTKPTA- 165
Db 251 SESEDESEDEETP-----KKKSDV-----EMVDAEKSSAQKPTPTSPAAG 294
Qy 166 -----AEIEDLSE 174
Db 295 GSKTLFAANLSFNIERADVENPFKE 319

RESULT 13
T40167
hypothetical protein SPBC30B4.01c - fission yeast (Schizosaccharomyces pombe) (fragment
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T40167; T40374
R/Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A.
submitted to the EMBL Data Library, August 1998
A/Reference number: Z21909
A/Accession: T40167
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-344 <LYN>
A/Cross-references: UNIPROT:P87179; EMBL:AL031262; PIDN:CAA20314.1; GSPDB:GN00067; SPDB
A/Experimental source: strain 972h-; cosmid c30B4
R/Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A.
submitted to the EMBL Data Library, December 1998
A/Reference number: Z21923
A/Accession: T40374
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 36-344 <WO>
A/Cross-references: EMBL:Z95620; PIDN:CA809116.1; GSPDB:GN00067; SPDB:SPBC3D6.14C
A/Experimental source: strain 972h-; cosmid c3D6
C/Genetics:
A/Gene: SPBC3D5.14C; SPDB:SPBC30B4.01c; SPDB:SPBC3D6.14C
A/Map position: 2

Query Match 11.1%; Score 116.5; DB 2; Length 344;
Best Local Similarity 32.1%; Pred. No. 1;
Matches 42; Conservative 19; Mismatches 57; Indels 13; Gaps 2;

RESULT 12
A96327
probable num1 protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence revision 02-Mar-2001 #text change 09-Jul-2004

